Result Ouery No. Score Match Length DB ID Description	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	<pre>Database : Issued_Patents_AA:*     1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*     2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*     3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*     4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*     5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*     6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*</pre>	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 9	Total number of hits satisfying chosen parameters: 66399	earched: 262574 seqs, 29422922 residues	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Title: US-09-625-963-1 Perfect score: 51 Sequence: 1 RMFPNAPYL 9	Run on: April 25, 2003, 06:57:10 ; Search time 13 Seconds (without alignments) 20.370 Million cell updates/sec	OM protein - protein search, using sw model	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	Fri Apr 25 08:06:19 2003
ORGANISM: Homo sapiens ; FEATURE: OTHER INFORMATION: Residues 96-104 of the PUMP-1 protein US-09-492-543-158	SOFTWARE: WORD 6.0.1 for Macintosh SEOFTWARE: WORD 6.0.1 for Macintosh LENGTH: 9 TYPE: PRT	TITLE OF INVENTION: COmpositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of FILE REFERENCE: D6223CIP-B CURRENT APPLICATION NUMBER: US/09/492,543A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: 09/039,211 PRIOR FILING DATE: 03-14-1998	Sequence 158, Application US/09492543A Patent No. 6316213 GENERAL INFORMATION:	RESULT 1	ALIGNMENTS	5 21 41.2 8 1 US-08-594-447-37 Sequence	2 2 41.2 7 2 US-U8-568-56-1.18 Sequence 3 21 41.2 7 4 US-09-367-940A-2 Sequence 4 21 41.2 7 5 PCT-US94-01321-69 Sequence	9       22       43.1       9       4       US-09-161-877B-25       Sequence         0       22       43.1       9       4       US-09-161-877B-25       Sequence         1       21       41.2       5       1       US-09-492-543-180       Sequence         1       21       41.2       5       1       US-07-880-216-1       Sequence	5         22         43.1         8         4         US-09-325-769-8         Sequence           6         22         43.1         8         4         US-09-636-170-7         Sequence           7         22         43.1         8         4         US-09-636-170-7         Sequence           9         22         43.1         8         4         US-09-636-170-7         Sequence           9         22         43.1         8         4         US-09-637-5188-75         Sequence	2 2 43.1 8 4 US-09-484-320-7 Sequence 3 22 43.1 8 4 US-09-484-321-7 Sequence 4 22 43.1 8 4 US-09-484-323-7 Sequence	28       23       45.1       8       5       PCT-US94-01321-70       Sequence 70, Appl         29       22       43.1       6       2       US-08-672-805-11       Sequence 11, Appl         30       22       43.1       8       4       US-09-484-318-7       Sequence 7, Appli         31       22       43.1       8       4       US-09-484-319-7       Sequence 7, Appli	25-963-1.closed.rai Page

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QY B RESULT 3 US-09-161-877B-26 Query Match Patent No. Sequence 26, Application US/09161877B Patent No. 6132980 Matches Best -09-162-368B-26 GENERAL INFORMATION: APPLICANT: WANG, R.F.; TITLE OF INVENTION: IDE TITLE OF INVENTION: AS TITLE OF INVENTION: CYT NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: TELEX: 421792 NFORMATION FOR SEQ ID NO: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/599,602 FILING DATE: 09-FEB-1996 ATTORNEY/ACENT INFORMATION: NAME: KATHRYN M. BROWN REGISTRATION NUMBER: 34,556 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK CURRENT APPLICATION DATA: FEATURE : SEQUENCE CHARACTERISTICS: TELEFAX: (212) 751-6849 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/725,736 FILING DATE: 04-0CT-1996 CURRENT APPLICATION DATA: MOLECULE TYPE: PRIOR APPLICATION DATA: COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOFT WORD 97 Local Similarity hes 4; Conserv OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOFT WORD 97 FILING DATE: 21 CLASSIFICATION: APPLICATION NUMBER: US/09 FILING DATE: 28-SEPT-1998 ZIP: COUNTRY : STATE : CITY: STREET : IDENTIFICATION METHOD: OTHER INFORMATION: NAME/KEY: STRANDEDNESS: TOPOLOGY: UN TYPE: REFERENCE/DOCKET NUMBER: CLASSIFICATION: FILING DATE: APPLICATION NUMBER: MEDIUM TYPE: COMPUTER: I ADDRESSEE : LOCATION: JENGTH: 9 TYDE: AMINO, ACID DESCRIPTION: PEPTIDE 2 LFPGRPY 8 2 MEPNAPY 8 10154 NEW YORK NEW YORK **345 PARK AVENUE** USA WANG, R.F.; ROSENBERG, S. A. VENTION: IDENTIFICATION OF TRP-2 VENTION: AS A HUMAN TUMOR ANTIGEN RECOGNIZED BY VENTION: CYTOTOXIC T LYMPHOCYTES Conservative UNKNOWN MORGAN & FINNEGAN, L.L.P IBM PC COMPATIBLE FLOPPY DISK 28-SEPT-1998 UNKNOWN 530 54.9%; 57.1%; 530 32 US/09/161,877B US/09/162,368B 34,556 ER: 202 26: 1. 2026-4243US1 Score 28; Pred. No. Mismatches 2e+05; DB 3; N Length 9; Indels 0; Gaps 0 B US-08-737-085A-6 RESULT 4 QY ; IDENTIFICATION METHOD ; OTHER INFORMATION: US-09-161-877B-26 Sequence 6, Application US/08737085A patent No. 5869232 GENERAL INFORMATION: APPLICANT: SALLBERG, MATTI Best Local Similarity Matches 4; Conserv Query Match TELEFAX: (212) 751-6849 TELEX: 421792 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: ATTORNEY/AGENT INFORMATION: NAME: Green, Reza REGISTRATION NUMBER: 38,475 REFERENCE/DOCKET NUMBER: 3846/0C569 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-527-7659 TELEFAX: 212-753-6237 ALC: STREET: BUC CITY: New York STATE: New York IISA CLASSIFICATION: 426 PRIOR APPLICATION DATA: APPLICATION NUMBER: COMPUTER READABLE FORM: MEDIUM TYPE: Diskett FILING DATE: 04-OCT-1990 FILING DATE: 04-OCT-1990 PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: 08/599,602 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: TITLE OF INVENTION: TITLE OF INVENTION: APPLICATION NUMBER: 08/5 FILING DATE: 09-FEB-1996 ATTORNEY/AGENT INFORMATION: NUMBER OF SEQUENCES: TELEPHONE: (212) 758-4800 FEATURE : TOPOLOGY: UNKNOWN WOLECULE TYPE: COMPUTER: IBM CON OPERATING SYSTEM: NAME/KEY: LOCATION: APPLICATION NUMBER: US/08/737,085A FILING DATE: 27-DEC-1996 FILING DATE: ZIP: NAME: KATHRYN M. BROWN REGISTRATION NUMBER: 3 TELEX : ADDRESSEE : DESCRIPTION: APPLICATION NUMBER: STRANDEDNESS : 2 LFPGRPY 8 2 MFPNAPY 8 LENGTH : 10022 AMINO ACID 236687 805 Third Avenue Conservative IBM Compatible DARBY & DARBY PC Diskette PEPTIDE UNKNOWN DOS 54.9%; 57.1%; EXCHANGER ANTIGEN/ANTIBODY SPECIFICITY 08/725,736 34,556 26: 1; 2026-4243US2 Score 28; DB 4; Pred. No. 2e+05; Mismatches DB 4; Length 9; 2 Indels 0 Gaps

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QY 4 PNAPYL 9 Db 2 PNAPIL 7 RESULT 6	Query Match 52.9%; Score 27; DB 3; Length 8; Best Local Similarity .83.3%; Pred. No. 2e+05; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	6 1 KE	REGISTRATION NUMBER: 3844/0C569 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-527-7659 TELEPHONE: 212-753-6237 TELEX: 236687	APPLICATION NUMBER: 08/737,085 FILING DATE: ATTORNEY/AGENT.INFORMATION: NAME: Green, Reza	CURKEWI APPLICATION DATA: APPLICATION NUMBER: US/09/246,258 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA.	MEDJUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEO for Windows Version 2.0	STATE: New York Country: USA ZIP: 10022 Computer Readable form:	CORRESPONDENCE ADDRESS: ADDRESSEE: DARBY & DARBY PC STREET: 805 Third Avenue CITY: New York	GEVERAL INFORMATION: APPLICANT: SALLBERG, MATTI TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY TITLE OF INVENTION: EXCHANGER NUMBER OF SEQUENCES: 23	RESULT 5 US-09-246-258-6 ; Sequence 6, Application US/09246258 ; Patent No. 6040137	4 PNAPYL 9        2 PNAPIL 7	Query Match 52.9%; Score 27; DB 2; Length 8; Best Local Similarity 83.3%; Pred. No. 2e+05; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 8 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide 08-737-085A-6	Fri Apr 25 08:06:19 2003 us-09-625-96
COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS	CURRESPONDENCE ADDRESS: ADDRESSEE: DARBY & DARBY PC STREET: 805 Third Avenue CITY: New York	US-09-339-666-6 ; Sequence 6, Application US/09839666 ; Patent NO. 6469143 ; GENERAL INFORMATION: ANTTI ; APPLICANT: SALLBERG, MATTI ; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY ; NUMBER OF SEQUENCES: 23	QY 4 PNAPYL 9 Db 2 PNAPIL 7 RESULT 7	Query Match 52.9%; Score 27; DB 4; Length 8; Best Local Similarity 83.3%; Pred. No. 2e+05; Matches 5; Conservative 0; Mismatches 1; Indels 0;	; TOPOLOGY: linear ; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-532-106-6	<u>S</u>	; TELEPHONE: 212-527-7659 ; TELEFAX: 212-753-6237 ; TELEX: 236687 ; INFORMATION FOR SEO ID NO: 6:	; NAME: Green, Reza ; REGISTRATION NUMBER: 38,475 ; REFERENCE/DOCKET NUMBER: 3846/0C569 ; TELECOMMUNICATION INFORMATION.	; FILING DATE: 21-Mar-2000 ; PRIOR APELICATION DATA: ; APELICATION NUMBER: US/08/737,085A ; FILING DATE: 27-DEC-1996 ; ATTORNEY/AGENT INFORMATION:	CONFUTER: IBM CONPOLITE COPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/532,106	COMPUTER READABLE FORM: COMPUTER READABLE FORM:	ADDRESSEE: DARBY & DARBY PC STREET: 805 Third Avenue CITY: New York	US-09-532-106-6 ; Sequence 6, Application US/09532106 ; Patent NO. 6245895 ; GENERAL INFORMATION: APPLICANT: SALLBERG, MATTI ; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY ; NUMBER OF SEQUENCES; 23 ; NUMBER OF SEQUENCES; 23	us-09-625-963-1.closed.rai
				Gaps										Pag

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Query Match Best Local Similarity Workshes 5; Conserva B QY US-09-839-666-6 **JS-08-672-805-12** RESULT Sequence Patent No. GENERAL INFORMATION: TELEX: 236 INFORMATION FOR SEQ OPERATING SYSTEM: DOS SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08, CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: COMPUTER READABLE FORM: NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: TITLE OF INVENTION: TITLE OF INVENTION: APPLICANT : APPLICANT : REFERENCE/DOCKET NUMBER: MSB-7236 TELECOMMUNICATION INFORMATION: TELEEMHONE: (510)705-7910 ATTORNEY/AGENT INFORMATION: APPLICANT : APPLICANT : œ MEDIUM TYPE: Diskette, COMPUTER: IBM STREET: 800 Dwight. STREET: P. O. Box 1 NAME: Giblin, James A. REGISTRATION NUMBER: 2 FILING DATE: FILING DATE: COUNTRY: USA ZIP: 94701-1986 STATE: California CITY: 4 PNAPYL 9 ADDRESSEE : 2 PNAPIL 7 REFERENCE/DOCKET NUMBER: 3846/0C569 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-527-7659 MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: SEQUENCE CHARACTERISTICS: PRIOR APPLICATION DATA: CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: 12, Berkeley 2, Application US/08672805 5831003 APPLICATION NUMBER: US/09/839,666 FILING DATE: 19-Apr-2001 TOPOLOGY: linear STRANDEDNESS: single TYPE: APPLICATION NUMBER: 08/737,085 FILING DATE: <Unknown> CLASSIFICATION: SOFTWARE: FastSEQ for Windows Version 2.0 LENGTH : TELEFAX: 212-753-6237 REGISTRATION NUMBER: 38,475 NAME: Green, Reza Buettner, Joseph A., Dadd, Christopher A., Hammond, David J. Baumbach, George A., Conservative Bayer Corporation H: 8 amino acids amino acid 236687 Box 1986 ID NO: 6: 52.98; 83.38; Thrombin Peptides Which Bind to Prothrombin and Wa 21 US/08/672,805 25772 <Unknown> 3.50 inch, 1.44Mb Storage 0 ;; Score 27; DB 4; Pred. No. 2e+05; 0; Mismatches б.: DB 4; 1. Length 8; Indels <u>,</u> Gaps 0 g RESULT 9 US-08-540-922D-8 B ; DESCRIPTION: US-08-672-805-12 Sequence 8, Application US/08540922D Patent No. 6284476 Query Match 51. Best Local Similarity 83. Matches 5; Conservative GENERAL INFORMATION: TELEFAX: (510)705-7904 INFORMATION FOR SEQ ID NO: TELEFAX: (2 NFORMATION FOR COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc APPLICATION NUMBER: 08/054,714 FILING DATE: 28 April 1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/540,922D FILING DATE: OCTOBER 11,1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA: MOLECULE TYPE: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200 FILING DATE: 22 December ATTORNEY/AGENT INFORMATION: SOFTWARE: Wordperfect CURRENT APPLICATION DATA: TITLE OF INVENTION: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS CORRESPONDENCE ADDRESS : APPLICANT : MOLECULE TYPE: DESCRIPTION: NUMBER OF SEQUENCES: APPLICANT : APPLICANT: APPLICANT : COMPUTER: IBM PS/ OPERATING SYSTEM: TYPE: amino STRANDEDNESS: APPLICATION NUMBER: 07/994,92 FILING DATE: 22 December 1992 REGISTRATION NUMBER: 36,669 REFERENCE/DOCKET NUMBER: LUD 5299.5 MEDIUM TYPE: COUNTRY : STATE : STREET : TOPOLOGY : NAME : ZIP: CITY: ADDRESSEE : TOPOLOGY : STRANDEDNESS : TYPE: LENGTH: 4 PNAPYL 9 LENGTH: 1 PFAPYL 6 10022 amino acid arrino strand amino acids New York Mary Anne Schofield New York 805 Third Avenue (212) 838-3884 OR SEQ ID NO: USA Boon-Falleur, Thierry; Brichard, Vincent; Van Pel, Aline; De Plaen, Etienne; Coulie, Pierre; Lethe, Bernard Renauld Jean-Christope; Wolfel, linear IBM PS/2 Felfe & Lynch peptide Protein single inch 1.44 Mb storage diskette 51.0%; 83.3%; INDIVIDUALS METHOD OF IDENTIFYING INDIVIDUALS SUFFERING FROM A CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN PC-DOS PEPTIDES, LEUKOCYTE ANTIGEN 12 07/994,928 12: æ 0 Score 26; Pred. No. AND METHODS Mismatches 2e+05; TYROSINASE DERIVED DB 2; FOR Thomas; and .. Length 6; TREATING SAID Indels 0 Gaps

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/ Sequence 28, Application US/09162368B
/ Patent No. 6083703 QY RESULT 11 US-09-162-368B-28 망 ; "TFEATURE: ; OTHER INFORMATION: ; OTHER INFORMATION: US-08-540-922D-8 뭥 Ş RESULT 10 PCT-US94-03744-6 PCT-US94-03744-6 Query Match Best Local : Matches GENERAL INFORMATION: Best Matches Query Match TELEFAX: (202) 887-0763 TELEX: 90-4030 INFORMATION FOR SEQ ID NO: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SEQUENCE CHARACTERISTICS: LENGTH: 8 amino acids TYPE: amino acid REGISTRATION NUMBER: 29,959 REFERENCE/DOCKET NUMBER: 29 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: FILING DATE: 09-APR-1993 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 1 CORRESPONDENCE ADDRESS TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: APPLICANT: APPLICANT: APPLICANT : STREET: CITY: V Local Similarity STRANDEDNESS : FILING DATE: CLASSIFICATION: TOPOLOGY : STATE : APPLICATION NUMBER: COUNTRY : ADDRESSEE : Local Similarity 57.: es 4; Conservative 3 PNYPY 7 4 PNAPY 8 ZIP: 2 FPLSPYV 8 3 FPNAPYL 9 OF SEQUENCES: 4; 20006-1812 Washington MURASHIGE, KATE H. Application PC/TUS9403744 R Morrison & Foerster
 2000 Pennsylvania Avenue, Suite 5500 Conservative USA MCCOY, JAMES J. MANN, BARBARA J. PETRI, WILLIAM A. linear single 49.0%; 80.0%; HISTOLYTICA ADHERENCE LECTIN 35/31 KDA SUBUNIT OF THE ENTAMOEBA 51.0%; 57.1%; SEQ of aa nt of SEQ US 08/045,679 PCT/US94/03744 <u>б</u>.: 29148-20005.00 0 ;; Score 26; DB Pred. No. 2e+( 2; Mismatches 2 Score 25; DB 5; Pred. No. 2e+05; Mismatches corresponding to nt 1816-1839 ID NO: 1 DB 4; 2e+05; <u>+</u> <u>ب</u> Length 8; Length 8; Indels Indels 0 0 Gaps Gaps 0 0

RESULT 12 US-09-161-877B-28 B ŝ US-09-162-368B-28 Sequence 28, Application US/09161877B Patent No. 6132980 Matches Query Match Best Local GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: WANG, R.F. TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: INFORMATION FOR SEQ ID NO: REGISTRATION NUMBER: 34,556 REFERENCE/DOCKET NUMBER: 20 TELECOMMUICATION INFORMATION: TELEPHONE: (212) 758-4800 TELEFAX: (212) 751-6849 FILING DATE: 09-FEB-1996 ATTORNEY/AGENT INFORMATION: NAME: KATHRYN BROWN CORRESPONDENCE ADDRESS: FEATURE : MOLECULE TYPE SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: 08/7: FILING DATE: 04-OCT-1996 PRIOR APPLICATION DATA: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOFT WORD 97 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/162,368B COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: PRIOR APPLICATION DATA: APPLICANT : Local Similarity hes 4; Conserv IDENTIFICATION METHOD: OTHER INFORMATION: FILING DATE: 28 CLASSIFICATION: LOCATION NAME/KEY: DESCRIPTION: STRANDEDNESS : TYPE: TELEX : APPLICATION NUMBER: 08/5 FTLING DATE: 09-FEB-1996 OPERATING SYSTEM: COMPUTER : STREET : TOPOLOGY : ZIP: STATE : CITY: STREET : ADDRESSEE : COUNTRY : ADDRESSEE : 4 PGAPY 8 4 PNAPY 8 ENGTH: 10154 NEW YORK NEW YORK 421792 AMINO ACID 345 PARK AVENUE **345 PARK AVENUE** WANG, R.F.; ROSENBERG, S. A. VVENTION: IDENTIFICATION OF TRP-2 AS VVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T VVENTION: LYMPHOCYTES USA Conservative UNKNOWN IBM PC COMPATIBLE MORGAN & FINNEGAN, L.L.P MORGAN & FINNEGAN, L.L.P. FLOPPY DISK PEPTIDE 28-SEPT-1998 UNKNOWN R.F.; ROSENBERG, S. A. N: IDENTIFICATION OF TRP-2 N: AS A HUMAN TUMOR ANTIGEN • 49.0%; 80.0%; CYTOTOXIC T LYMPHOCYTES 08/725,736 08/599,602 28: <u>,</u> Score 25; Pred. No. 2026-4243US1 Mismatches 2e+05; DB 3; RECOGNIZED <u>г</u> Length 9; Indels ВΥ <u>,</u> Gaps 0

Query Match Best Local Similarity Matches 4; Conserv? 뭥 Q RESULT 13 US-08-261-525A-6 US-09-161-877B-28 Sequence 6, Application US/08261525A Patent No. 5569598 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: REGISTRATION NUMBER: 34,556 REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800 TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FEATURE : TOPOLOGY: MOLECULE TYPE SEQUENCE CHARACTERISTICS: FILING DATE: 09-FEB-1996 ATTORNEY/AGENT INFORMATION: CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: APPLICANT : APPLICANT : APPLICANT : PRIOR APPLICATION DATA: APPLICANT : APPLICANT : APPLICANT : PRIOR APPLICATION DATA: APPLICANT : IDENTIFICATION METHOD: OTHER INFORMATION: TYPE: AMINO ACID STRANDEDNESS: UNK TOPOLOGY: UNKNOWN APPLICATION NUMBER: FILING DATE: 28-SEI CLASSIFICATION: 53( CITY: Daejeon STATE: Daejeon DESCRIPTION: PEPTIDE TELEX : APPLICATION NUMBER: 08/725,736 FILING DATE: 04-OCT-1996 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOFT WORD 97 TELEFAX : COUNTRY : CITY: NEW YORK 4 PNAPY 8 NAME/KEY: APPLICATION NUMBER: COMPUTER : STATE: STREET : ADDRESSEE : 4 PGAPY 8 LOCATION ENGTH : NAME : KATHRYN M. BROWN 10154 (: (212) 751-6849 421792 NEW YORK Daejeon E: PARK, Soon Jae Lucky Apt. 6-101, Doryong-dong, Yuseong-gu PARK, Soon Jae LEE, Young Mee WON, Teug Yeon KWON, Soon Chang LEEE, Seung Joo KIM, Jung Ho KIM, Jung Ho KIM, Bum Joon Conservative USA IBM PC COMPATIBLE 28-SEPT-1998 UNKNOWN 49.0%; 80.0%; PROTEIN THEREFROM 08/599,602 US/09/161,877B 28: 0 2026-4243US2 Score 25; DB 4; Pred. No. 2e+05; Mismatches DB 4; 1; Indels Length 9; 0; Gaps 0

US-08-261-525A-6 Matches Query Match Best Local Similarity APPLICATION NUMBER: US/08/261,525 FILING DATE: 17-JUN-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: KR 93-11107 FILING DATE: 17-JUN-1993 ATTORNEY/AGENT INFORMATION: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: OPERATING SYSTEM: MS-DOS SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: MOLECULE TYPE: COMPUTER READABLE FORM: COUNTRY: Ner-TYPE: MEDIUM TYPE: Flop COMPUTER: IBM PC/ OPERATING SYSTEM: COUNTRY: Rep 7TP: 302-181 TOPOLOGY : TELEFAX: TELEPHONE: **REGISTRATION NUMBER:** COUNTRY: Republic of Korea ZIP: 305-340 CITY: Daejeon STATE: Daejeon STREET: Lucky Dormitory 502, 386-1, Doryong-dong, STREET: Yuseong-gu ADDRESSEE: KIM, Jung Ho STREET: Lucky Dormitory 511, 386-1, Doryong-dong, STREET: Viscong-gu COUNTRY: Republic of Korea ZIP: 305-340 ADDRESSEE: LEE, Seung Joo STREET: Lucky Apt. B-107, 386-4, Doryong-dong, STREET: Yuseong-gu COUNTRY: Republic of Korea ZIP: 302-181 CITY : STREET: Gongjak Hanyang Apt. STREET: Tanbang-dong, Seo-gu STREET: Shins CITY: Daejeon NAME : ADDRESSEE : STATE: CITY: STATE: CITY: STATE : STREET : ADDRESSEE : STATE : CITY: STATE : ZIP: COUNTRY : ADDRESSEE : ZIP: ENGTH: ADDRESSEE : 2 MEPNAP 7 4; 302-223 Daejeon Daejeon Daejeon 305-340 Daejeon amino acid Shahan Islam Daejeon Daejeon Daejeon Daejeon Daejeon E: LEE, Young Mee Shinsung Apt. 3-306, E: KWON, Soon Chang Shinsung Apt. 3-107, 7 amino acids Conservative (212) Republic of Korea Republic of Korea Republic of Korea 3: Floppy disk, 3.5 inch, 1.44MB storage IBM PC/AT linear KIM, Bum Joon WON, Teug Yeon (212) 278-1000 peptide 953-7249 ID NO: 6: 47.18; 66.78; US/08/261,525A 32,507 <u>,</u> Score 24; DB 1; Pred. No. 2e+05; A-9883 Mismatches 28-4, Nae-dong, Seo-gu 28-4, Nae-dong, Seo-gu 3-1201, 835 ຸ ເ Length 7; Indels 0 Gaps

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Ъ ş 닳 US-08-417-174-13 RESULT 15 RESULT 14 US-09-367-940A-1 US-09-367-940A-1 Sequence 13, Application US/08417174 Patent No. 5844075 Query Match Best Local S Sequence 1, Application US/09367940A Patent No. 6428997 GENERAL INFORMATION: Matches Fri Apr 25 08:06:19 2003 GENERAL INFORMATION: APPLICATION NUMBER: US/09/367,940A FILING DATE: 18-Aug-1999 INFORMATION FOR SEQ ID NO: 1 : SEQUENCE CHARACTERISTICS: LENGTH: 7 amino acids TYPE: amino acid STRANDEDNESS: single à NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, APPLICANT: STEVEN A. TITLE OF INVENTION: MELANOMA ANTIGENS AND TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC TITLE OF INVENTION: METHODS ZIP: 10154 COMPUTER READABLE FORM: Local Similarity 66. les 4; Conservative STREET : CITY: COUNTRY : STATE : ADDRESSEE : 1 MFPTEP 6 2 MFPNAP 7 1 MFPTEP ZIP: 06510-2802 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage TITLE OF INVENTION: Aminopeptidase derived from Bacillus licheniformis and process for proparation of natural CORRESPONDENCE ADDRESS: 4 CORRESPONDENCE ADDRESS: 4 ADDRESSEE: BACHMAN & LAPOINTE, P.C. STREET: Suite 1201, 900 Chapel Street MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 1 CURRENT APPLICATION DATA: APPLICANT: LG CHEMICAL LTD -T: 345 PARK AVENUE NEW YORK OPERATING SYSTEM: WINDOWS 95/98 SOFTWARE: MS WORD CITY: New Haven STATE: Connecticut TOPOLOGY: linear COMPUTER: IBM COUNTRY: U.S.A. NEW YORK USA σ MORGAN & FINNEGAN, L.L.P. LEE, Young-Ph HAN, Kyuboem KIM, Se-Hoon Se-Hoon Young - Phil 47.18; 66.78; 126 Score 24; DB Pred. No. 2e+0 0; Mismatches 0 DB 4; Length 7; 2e+05; 2 Indels 0 ;; Gaps 0 많 Q

Query Match Best Local Similarity Arches 4; Conserve ; TOPOLOGY: U ; MOLECULE TYPE: US-08-417-174-13 Search completed: April 25, 2003, 06:59:31 Job time : 14 secs REGISTRATION NUMBER: 37,341 REFERENCE/DOCKET NUMBER: 2028 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800 TELEFAX: (212) 751-6849 TELEFAX: (212) 751-6849 TELEX: 421792 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: NAME: CAROL M. GRUPPI PRIOR APPLICATION DATA: APPLICATION NUMBER: US/O FILING DATE: 22-APR-1994 STRANDEDNESS: TYPE : APPLICATION NUMBER: FILING DATE: 05-AP LENGTH : CLASSIFICATION: MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE COMPUTER: 4 PNAP 7 4 PNAP 7 amino acid Conservative Unknown Peptide 05-APR-1995 Unknown 435 47.1%; Score 24; DB 100.0%; Pred. No. 2e+ Live 0; Mismatches US/08/231,565 US/08/417,174 2026-4124US1 , DB 2; ... .o. 2e+05; 0; Length 9; Indels 0 ;; Gaps

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Page J . .

1       19       37.3       9       2       S70345       AmFase R1 subunit         2       18       35.3       9       2       S70345       AmFase R1 subunit         3       17       33.3       9       2       S70345       AmFase R1 subunit         3       17       33.3       9       2       S70345       AmFase R1 subunit         4       17       33.3       9       2       H4108       Ig heavy chain vr         5       17       33.3       9       2       S0302       xenopsin-related p         6       17       33.3       9       2       H00320       cathon-nonoxide de         10       16       31.4       7       2       S21230       gene Cftr pretein         11       15       29.4       9       2       Ad1978       guinoline 2-oxidor         11       15       29.4       9       2       H61620       Ig Haras S'-regi         12       14       27.5       8       2       H47393       neuroperin I       Ig Horistav Crobin -         14       27.5       8       2       H47393       neuroperide calla       inulinase (EC 3.2)         14 <th>SUMMARIES Query Match Length DB ID</th> <th>Database : pIR_73:* 1: pir1:* 2: pir2:* 3: pir2:* 4: pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.</th> <th>Total number of hits satisfying chosen parameters: 789 Minimum DB seq length: 0 Maximum DB seq length: 9 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</th> <th>Gapop 10.0 , Gapext 0.5 Searched: 283224 seqs, 96134422 residues</th> <th>-625-963-1 PNAPYL 9 M62</th> <th>(c) 1993 - 2003 , using sw model 2003, 06:51:39 ; se 61</th> <th>Fri Apr 25 08:06:20 2003 us-09-625-963-1.closed.</th>	SUMMARIES Query Match Length DB ID	Database : pIR_73:* 1: pir1:* 2: pir2:* 3: pir2:* 4: pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Total number of hits satisfying chosen parameters: 789 Minimum DB seq length: 0 Maximum DB seq length: 9 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Gapop 10.0 , Gapext 0.5 Searched: 283224 seqs, 96134422 residues	-625-963-1 PNAPYL 9 M62	(c) 1993 - 2003 , using sw model 2003, 06:51:39 ; se 61	Fri Apr 25 08:06:20 2003 us-09-625-963-1.closed.
SULT 2 8186 R1 Subuni Species: Nicot Date: 16-Feb1 Date: 16-Feb1 Date: specifi Title: Specifi Title: Specifi Title: Specifi Status: prelim Molecule type: Residues: 1-9 Experimental s Note: sequence Note: sequence Note: sequence Note: sequence Note: sequence Note: Sequence SULT 3	al similarity 60.0%; pred. NO. 2.8e+05; 3; Conservative 0; Mismatches 2 PNAPY 8 PNAPY 8	AKU 3302 contain topa qui 9675 Length 9;	RESULT 1 S70345 amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments) C;Species: Aspergillus niger C;Dece: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998 C;Accession: S70345 C;Accession: S70345 R;Frebort, I.; Pec, P.; Luhova, L.; Toyzma, H.; Matsushita, K.; Hirota, S.; Kitagawa,	SIMENTS	13     25.5     8     2       13     25.5     8     2       13     25.5     8     2       13     25.5     8     2       13     25.5     8     2       13     25.5     8     2       13     25.5     8     2       13     25.5     8     2	32       13       25.5       7       2       A153210       gene c-rel protein         33       13       25.5       7       2       E48394       glycoprotein compo         34       13       25.5       7       2       E48394       glycoprotein compo         35       13       25.5       8       2       S08995       hypertrehalosemic         36       13       25.5       8       2       S08996       hypertrehalosemic         37       13       25.5       8       2       A49823       adipokinetic hormo         38       13       25.5       8       2       B49823       adipokinetic hormo         39       13       25.5       8       2       B49823       adipokinetic hormo         39       13       25.5       8       2       B49823       adipokinetic hormo         30       13       25.5       8       2       B49820       adipokinetic hormo	Interpretation         Pag           13         25.5         6         2         A61049         halo-toxin - Pse           13         25.5         6         2         A44916         mosquitocidal to

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Page 2

<pre>RESULT 5 A60320 xeenopsin-related peptide 2 - rat N:Contains: xeenopsin-related peptide 1 C:Species: Rattus norvegicus (Norway rat) C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Aug-2000 C:Accession: A60320 R:Carraway, R.E.; Mitra, S.P.; Muraki, K. Regul. Pept. 29, 229-239, 1990 R:Carraway, R.E.; Mitra, S.P.; Muraki, K. Reference number: A60320; MUID:91018491; PMID:2217904 A:Reference number: A60320; MUID:91018491; PMID:2217904 A:Molecule type: protein A:Residues: 1-9 <car></car></pre>	<pre>;2-9/Product: xenopsin-related peptide 1 #status experimental Query Match 33.3%; Score 17; DB 2; Length 9; Best Local Similarity 33.3%; Pred. No. 2.8e+05; Matches 2; Conservative 2; Mismatches 2; Indels y 4 PNAPYL 9 1 1:: b 3 PKRPWI 8</pre>	JS0302 JS0302	د م	Query Match 33 Best Local Similarity 75 Matches 3; Conservativ	<pre>PH1408 Ig heavy chain V region - mouse (fragment) C:Species: Mus musculus (house mouse) C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999 C:Accession: PH1408; PH1405; PH1405; I agiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta A:Fitle: Heavy chain variable (VH) region diversity generated by VH gene replacement in a virus. A:Reference number: PH1403; MUID:93018837; PMID:1402663 A:Accession: PH1408 A:Accession: PH1408 A:Acces</pre>	
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RESULT 8 I57018 gene Cftr protein - mouse (fragment) C;Species: Mus sp. (mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997 C;Accession: I57018	Query Match 31.4%; Score 16; DB 2; Length 7; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	<pre>RESULT 7 S21230 dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment) c:Species: Phyllomedusa bicolor (two-colored leaf frog) C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000 C:Accession: S21220 R;Mignogna, G; Severini, C:; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, FEBS Lett. 302, 151-154, 1992 A;Title: Identification and characterization of two dermorphins from skin extracts of A;Accession: S21220; MUID:92339502; PMID:1633846 A;Status: preliminary A;Residues: 1-7 <mig> A;Residues: 1-7 <mig> </mig></mig></pre>	Qy 5 NAP 7 111 Db 2 NAP 4	<pre>Query Match 33.3%; Score 17; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	genase	PLO139 Hugendieck, I.; Herwig, S.; ol. 152, 335-341, 1989 logy and distribution of CO unber: PL0138; MUID:90055672		QY 4 PNAPYL 9    : Db 3 PKRPWI 8	Query Match 33.3%; Score 17; DB 2; Length 9; Best Local Similarity 33.3%; Pred. No. 2.8e+05; Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	A;Note: the authors purified these peptides from pepsin-treated extracts of stomach, C;Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in seque C:Superfamily: yeast coatomer complex alpha chain; WD repeat homology C;Keywords: neuropeptide F;1-9/Product: xenopsin-related peptide 2 #status experimental <mat1> F;2-9/Product: xenopsin-related peptide 1 #status experimental <mat2></mat2></mat1>
		<pre>Match 31.4%; Score 16; DB 2; Length 7; Scal Similarity 66.7%; Pred. No. 2.8e+05; 2; Conservative 1; Mismatches 0; Indels 0; Gaps</pre>	<pre>(Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment) Phyllomedusa bicolor (two-colored leaf frog) .war-1997 #sequence_revision 10-oct-1997 #text_change 18-Aug-2000 .: \$21230 .G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil 302, 151-154, 1992 entification and characterization of two dermorphins from skin extracts o number: \$21152; MUID:92339502; PMID:1633846 .: \$21230 Ly: dermorphin precursor; dermorphin precursor amino-terminal homology Ly: dermorphin precursor; dermorphin precursor amino-terminal homology .tsimilarity 66.7%; Pred. No. 2.8ee05; .toh .coh .coh .coh .coh .coh .coh .coh .c</pre>	<pre>AAP 7 II   II   II   II   II   II   II   II</pre>	<pre>cch 33.3%; Score 17; DB 2; Length 9; 1 Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0; 1, p7 1   1 1   1 1</pre>	<pre>n: PL0139 type: protein type: protein 1:9 <kra> Cardon-monoxide dehydrogenase consists of three polypeptide chains: large oxidoreductase 33.3%; Score 17; DB 2; Length 9; 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; AAP 7 11 AAP 7 11 AAP 7 11 (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment) Phyllonedusa bicolor (two-colored leaf frog (fragment) MAP 4 (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment) Phyllonedusa bicolor (two-colored leaf frog Nar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000 15: S21230 15: S21230 16: S202339502; PMID:1633846 19: S21230 19: S21152; MUID:32339502; PMID:1633846 19: S21230 19: S21230 19: dermorphin precursor; dermorphin precursor amino-terminal homology 19: lsimlarity 66.7%; pred. No. 2.8e+05; 11: Simlarity 66.7%; pred. No. 2.8e+05; 12: Conservative 1; Mismatches 0; Indels 0; Gaps 0; 14: Similarity 12: Mismatches 0; Indels 0; Gaps 0; 15: S21230 15: S2130 15: S21230 15: S21230 15: S21230 15: S21230 15: S21230 15: S2130 15: S21230 15: S2130 15: S21230 15: S21230 15: S2130 15: S21230 15: S2130 15: S2130</kra></pre>	<pre>:: Hugendieck, I.; Herwig, S.; Meyer, O. ; Higendieck, I.; Herwig, S.; Meyer, O. pmology and distribution of CC dehydrogenase structural genes in carboxydo pmology and distribution of CC dehydrogenase structural genes in carboxydo pmology and distribution of CC dehydrogenase structural genes in carboxydo pmology and distribution of CC dehydrogenase structural genes in carboxydo pmology and distribution of CC dehydrogenase structural genes in carboxydo pmology and distribution of CC dehydrogenase consists of three polypeptide chains: large coxidor-monoxide dehydrogenase consists of two- conservative 0; Mismatches 0; Indels 0; Gaps 0; then is S1230 is Sill 154, 1992 Silmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil 302, 151-154, 1992 Silmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil 302, 151-154, 1992 Multi: 9239502; PMID: 1633846 is number: S21152; MUID: 9239502; PMID: 1633846 is structure 31.4%; Score 16; DB 2; Length 7; is sillarity 66.7%; Pred. No. 2.8e+05; 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;</pre>	<pre>xxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydoflava Pseudomonas carboxydoflava sep-1990 #sequence_revision 07-sep-1990 #text_change 20-Apr-1993 ; Hugendieck, I.; Herwig, S.; Weyer, O. biol. 152, 33-34, 1989 ; number; Full38; MUID:90055678; PMID:2818128 type: protein l=</pre>	<pre>MAPFL 9</pre>	<pre>ch 33.3%; Score 17; DB 2; Length 9; 1 Similarity 33.3%; Score 17; DB 2; Length 9; 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0; NAPYL 9  :: 1 Nupendass carboxydoflava seeudomonas seeudomonas carboxydoflava seeudomonas carboxydoflava seeudomonas secure seeudomonas carboxydo secure seeudomonas seeudomonas seeudomonas secure seeudomonas carboxydo secure seeudomonas see</pre>

Query Match 29.4%; Score 15; DB 2; Length 9; Best Local Similarity 44.4%; Pred. No. 2.8e+05;	
ε, γγρατιτές στης: απιταικά σατροχγτ επα (τεα) φορατιο εχρειτημεπικάτ	Db 2 PNQDEM 7
ated carboxyl end; neuropeptide	Qy 4 PNAPYL 9
A;Status: pretruminary A;Rolecule type: protein A;Residues: 1-9 <sch></sch>	Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
A; Reference number: A01020 A; Accession: A61620	Aatch 31.48; Score 16;
nem. Mol. Biol. 22, 447-452, 1992	C:Keywords: amidated carboxyl end; neuropeptide F;9/Modified site: amidated carboxyl end (Phe) #status experimental
C;Accession: A61620 R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.	A;Molecule type: protein A;Residues: 1-9 <duv></duv>
C;Species: Locusta migratoria (migratory locust) C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997	A;Accession: D41978 A;Status: preliminary
A61620 Jocustamyotropin III – migratory locust	A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi A;Reference number: A41978; MUID:92196111; PMID:1549595
RESULT 13	R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
Db 3 FPAFAY 8	C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999 C:Accession: n41978
QY 3 FPNAPY 8	calliFMRFamide 4 - bluebottle fly (Calliphora vomitoria) C.Sporjae: Calliphora vomitoria
Query Match 29.4%; Score 15; DB 2; Length 9; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	RESULT 10
antal source: strain 63	Db 2 PNRDFM 7
Residues: 1-9	QY 4 PNAPYL 9
	Pred. No. 2.8e+05; 2; Mismatches 2
Eur. J. Biochem. 232, 536-544, 1995 A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase fr	Query Match 31.4%; Score 16; DB 2; Length 9;
C;Accession: S66607 R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.	C;Keywords: amidated carboxyl end; neuropeptide F;9/Modified site: amidated carboxyl end (Phe) #status experimental
C;Species: Comamonas testosteroni C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999	A;Molecule type: protein A;Residues: 1-9 <duv></duv>
S66607 quinoline 2-oxidoreductase beta chain • Comamonas testosteroni (fragment)	A;Accession: A44787 A;Status: preliminary
RESULT 12	A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi A;Reference number: A41978; MUID:92196111; PMID:1549595
Db 1 MAPSA 5	R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
QY 2 MFPNA 6	C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999 C;Accession: A44787
rative 1	calliFMRFamide 10 - bluebottle fly (Calliphora vomitoria) C;Species: Calliphora vomitoria
atch 29.4%; Score 15; DB 4; Length 6; cal Similarity 60.0%; Pred. No. 2.8e+05;	RESULT 9 A44788
A;Cross-references: GDB:120337; OMIM:180240 A;Map position: 17q12-17q12	Db 2 PDSP 5
	QY 4 PNAP 7
A;Cross-references: EMBL:X50058; NiD:43506 A;Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0 C:Comment: This sequence is not thought to be translated.	Pred. NO. 2; Mismat
A; Molecule type: DNA A; Residues: 1-6 	tch
	A;Gene: Cftr
Nucleic Acids Res. 18, 6799-6806, 1990 A;Title: Characterization of a functional promoter for the human retinoic acid recept h.Defense human retinoic acid recept	A;Residues: 1-8 <res> A;Cross-references: GB:S74246; NID:g710482</res>
C;Accession: S15596 R;Brand, N.J.; Petkovich, M.; Chambon, P.	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
pecies: H ate: 04-J	7018; MUID:95037043; PMID:7949729
s15596 orf 3 rara 5'-region - human	term survival of the exon 10
RESULT 11	in, J.R.
	)
.closed.rpr Page 3	Fri Apr 25 08:06:20 2003 us-09-625-963-1.closed.rpr

Fri Apr 25 08:06:20 2003

subesophageal ganglion pentapeptide - house cricket c;Species: Acheta domesticus (house cricket) G;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000 C;Accession: JS0319 R;Wicker, C.; Wicker, C. Comp. Biocchem. Physiol. C 88, 185-187, 1987 A;Title: Isolation and structure of a peptide isolated from the suboesophageal ganglion A;Fitle: Isolation and structure of a peptide isolated from the suboesophageal ganglion A;Fitle: Isolation and structure of a peptide isolated from the suboesophageal ganglion A;Accession: JS0319 A;Accession: JS0319 A;Molecule type: protein A;Residues: 1-5 <WIC> RESULT 15 JS0319 Db RESULT 14 PH1591 Ŷ QY A;Experimental source: bone marrow pre-B lymphocyte C;Keywords: immunoglobulin R;Levinson, D.A.; Campos-Torres, J.; Leder, P. J. EXP. Med. 178, 317-329, 1993 A;Tille: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PH1580; MUID:93301609; PMID:8315387 A;Accession: PH1591 A;Molecule type: DNA A;Residues: 1-9 <LEV> C;Date: 02-Ju C;Accession: B QY Search completed: April 25, 2003, 06:58:37 Job time : 16 secs B Ig H chain V-D-J region (wild-type clone 142) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999 Query Match 27.5 Best Local Similarity 66.7 Matches 2; Conservative Query Match 29.4 Best Local Similarity 66.7 Matches 2; Conservative Matches 6 APY 8 ||: 3 APF 5 6 APY 8 :|| 5 SPY 7 1 RMFPNAPYL 9 1 RQQPFVPRL 9 *ر*ار. 4; PH1591 Conservative 29.4%; Score 15; DB 2; Length 9; 66.7%; Pred. No. 2.8e+05; vative 1; Mismatches 0; Indels 27.58; 66.78; Score 14; DB 2; Le pred. No. 2.8e+05; 1; Mismatches 0; 0; Mismatches ა . Length 5; Indels Indels 0 0; Gaps 0; Gaps Gaps 0 <u>,</u> 0;

Page 4

32 32 32 32 33 34 35 35 35 35 35 35 35 35 35 35	Scc	Maximum DB seq 1 Post-processing: Database : Pred. No. score grea and is der	n mbe	Title: Perfect score: Sequence: Scoring table:	
22222222222222222222222222222222222222	%         Query         Match Length DB         43.1       9         35.3       7         35.3       7         35.3       7         35.3       9         33.3       9         33.3       9         33.3       9         31.4       9         31.4       9	ength: 9 Minimum Match 0% Maximum Match 100% Listing first 45 summaries SwissProt_40:* SwissProt_40:* is the number of results predicted is the number of results predicted ter than or equal to the score of t tved by analysis of the total score	112892 É hits sa Ìenath:	US-09-625-963-1 51 1 RMFPNAPYL 9 BLOSUM62 Gapop 10.0 , Gapext 0.5	GenCore versic opyright (c) 1993 - 2003 , n search, using sw model il 25, 2003, 06:51:04 ;
P801259 treponema h P801259 treponema h P801259 treponema h P801809 carcinus ma P41489 locusta mig P81806 carcinus ma P81807 carcinus ma P81807 carcinus ma P81807 carcinus ma P81808 carcinus ma P81819 carcinus ma P81819 carcinus ma P82125 cydia pomon P41840 calliphora P81811 carcinus ma P81812 carcinus ma P81813 carcinus obe P16339 thunnus obe P16339 thunnus obe P16339 thunnus obe P16339 locusta mig P16339 p04277 hono sapien	Description P90093 homo sapien P9025 mus musculu P81675 pinus pinus P8292 periplaneta P42997 scyliorhinu P80027 octopus vul P41855 calliphora	by chance to have a the result being printed, distribution.	231		n 5.1.4_p5_4578 3 Compugen Ltd. 3 Search time 25 Seconds (without alignments) 14.931 Million cell updates/sec
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<pre>matches 3; 7 AA. update) on update) atory protein atory protein atory tebration ata; Vertebration ata; Vertebration athi; Murid vertebration ognathi; Murid vertebration ognathi; Murid</pre>	., pjerrqvi crosequenci ;DETERMINED kDa kDa EB0772C7 CR EB0772C7 CR		f.	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	777 778888

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; Mismatches Score 18; Score 18; Pred. NO. PRT; PRT; 25 Mismatches THE DETERMINED 25 kDa. No. 1.1e+05 update) needle с., update) Bacteroidales; gingivalis) ω 7 DB 1; 1 DB AA AA REVERSED BY L-PHENYLALANINE .1e+05 Bahrman and <u>н</u> 0 2 Length 7; Length 7; xylem ΡI N., Indels Indels QF maritime Tracheophyta; THIS UNKNOWN Kremer 0; 0; A., pine Gaps Gaps 0 0 DT DT DT DT DT DT 망 Q SOTAR STATE RESULT RESULT D Ŷ SQ RT RT Query Match Best Local S Matches 4 Query Match Best Local S Matches 3 -\_SCYCA OXYF\_SCYCA P42997; 01-NOV-1995 01-NOV-1995 01-NOV-1995 Neuropeptide; MOD\_RES SEQUENCE 8 A P82692; 16-0CT-2001 16-0CT-2001 16-0CT-2001 Antigen. NON\_TER PERAM PPK2\_PERAM Phasvatocin the Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.; "Isolation and structural elucidation of two pyrokinins from retrocerebral\_complex of the American cockroach."; TISSUE=Corpora cardiaca; MEDLINE=97353923; PubMed=9210163; Blattoidea; InterPro; IPR001484; Pyrokinin.
PROSITE; PS00539; PYROKININ; FALSE\_NEG (MYOTROPIC ACTIVITY). -!- TISSUE SPECIFICITY: CORPORA CARDIACA Predel R., Eckert MEDLINE=20189894; TISSUE SPECIFICITY SEQUENCE, FUNCTION, NCBI\_TaxID=6978; Pyrokinin-2 (Pea-PK-2) (FXPRL-amide). Periplaneta americana (American cockroach). Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pteryyota; Neoptera; Orthopteroidea; Dictyoptera; Blattoidea; Blattidae; Periplaneta. SEQUENCE -1- MASS SPECTROMETRY: MW=883; METHOD=MAL -1- SIMILARITY: BELONGS TO THE PYROKININ ÷ "Tagma-specific distribution of FXPRLamides in Peptides 18:473-478(1997). N σ σ Comp. Neurol. 419:352-363(2000). - FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ω 4 PNAPYL ы σ American cockroach APY PFAPRL APY . Similarity 3; Conserv 4; Similarity ω œ ω (Rel. (Rel. (Rel. æ ø (Rel. 40, Created) (Rel. 40, Last sequence up (Rel. 40, Last annotation Conservative Conservative AA; AA; Amidation; Pyrokinin. œ æ STANDARD; STANDARD; 884 32, Created)
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 32, Last annotation updat . . 686 PubMed=10723010; 35.3%; ... 100.0%; Pr ... 0; AND MASS SPECTROMETRY 33.38; 66.78; æ æ MW ; MW; AMIDATION. C834176DD9D77775 CRC64; 9554540326CB476D CRC64; <u>,</u> Score 18; Pred. No. Pred. No. 1.1
); Mismatches Score 17; PRT; PRT; METHOD=MALDI Mismatches updaté) No. soluble whole update update) Ц ە æ DB 1; L 1.1e+05; DB 1; AA. 1e+05 FAMILY. A <u>.</u> 0 ₽ Length 8; the nervous system Length 8; Indels Indels ACTIVITY cell antigens Blattaria; Hexapoda; <u>,</u> 0 the Gaps Gaps of 0f .

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9 AA; 1183 MW;	QY 3 FPNAP 7
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RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992). CC -:- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)	SQ SEQUENCE 9 AA; 1072 MW; 17FF476EB45409DB CRC64;
	PROSITE; PS00264; NEU Hormone; Amidation. DISTLETD 1
RA MEULINE=YIY9111, PUDMEd=1349595; RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., RA Rehfeld J.F., Thorpe A.;	InterPro; Pfam; PF0
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OC Insecta; Pterygota; Neoptera; Bndopterygota; Diptera; Brachycera; OC Muscomorpha; Oestroidea; Calliphoridae; Calliphora.	"A r
Calliphora vomitoria (Blue blowfly). Fukarvota: Metaroa: Arthropoda: Mandibulata: Danorustacea:	RX MEDLINE=92270139; PubMed=1589145; RA Reich G.:
DT 01-WOV-1995 (Rel. 32, Last sequence update) DT 01-WOV-1995 (Rel. 32, Last annotation update)	RP SEQUENCE.
P41865; 01-NOV-1995 (Rel. 32,	Incirrata; Octopodidae; Octopus. NCBI_TaxID=6645;
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OY 4 PNAPYL 9	OXYT_OCTVU STANDAR P80027;
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Rehfeld J.F., Thorpe A. "Isolation, structure,	D 1 6
MEDLINE=92196111; Pur Duve H., Johnsen A.H	
RC TISSUE=Thoracic ganglion;	
NCBI_Tax	
a; Neoptera; Endopterygota; Diptera; Brac) roidea; Calliphoridae; Calliphora.	<pre>RT isolated from the spotted dogfish (Scyliorhinus caniculus)."; RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).</pre>
Callipho Eukaryoti	"Special evolution of neurohypophysial hormones in cartila fishes: asvatocin and phasvatocin, two oxytocin-like pepti
01-NOV-1995 (Rel. 32, CalliFMRFamide 4.	MEDLINE=95062247; Pub Chauvet J., Rouille Y
DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update)	RD SEQUENCE. RC TISSUE-Pituitary;
24	NCBI_TaxID=7830
<b>F</b>	<pre>OS Scyfforhinus canicula (Spotted dogfish) (Spotted catshark). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; OC Elasmobranchii; Galeonorphii; Galeoidea; Carcharhiniformes; OC scyliophinae, scyliophine;</pre>
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UPA3. 밇 QY FLA2 ID 망 QY RESULT 11 AC RESULT Best Loc Matches Query Match Best Local Matches 01-FEB-1995 16-OCT-2001 Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H. van der Zeijst B.A.M., Kusters J.G.; "The periplasmic flagella of Serpulina (Treponema) composed of two sheath proteins and three core prot J. Gen. Microbiol. 138:2697-2706(1992). "Plasma protein map: an update by microsequencing."; Electrophoresis 13:707-714(1992). -i- MISCEL,ANEOUS: ON THE 2D-GEL THE DETERMINED PI O MEDLINE-93092937; PubMed=1459097; Hughes G.J., Frutiger S., Paquet N., R Sanchez J.-C., James R., Tissot J.-D., Hochstrasser D.F.; HUMAN -!- SUBCELLULAR Flagella; Peripl Treponema hyodysenteriae Bacteria; Spirochaetales; NCBI\_TaxID=159; TISSUE=Plasma; SEQUENCE Eukaryota; Metazoa; Homo sapiens (Human). Unknown protein 01-APR-1993 16-OCT-2001 01-APR-1993 P30089; UPA3\_HUMAN SEQUENCE NON\_TER UNSURE UNSŪRE MEDLINE=93139764; STRAIN=C5 SEQUENCE TREHY NCBI\_TaxID=9606; Mammalia; Eutheria; ÷ FLAA2 Flagellar filament FLA2\_TREHY ÷ P80159; Fragment). 10 Local 7 PYL -FEB-1995 4 N 4 FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA. SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF SHEATH PROTEINS, FLAAL (14 kDa) AND FLAA2 (35 kDa) AROUND A CC THAT CONTAINS THREE PROTEINS FLABL (37 kDa), FLAB2 (34 kDa) AN РҮМ FLAB3 (32 kDa) || :: PNRDFM PNAPYL Similarity 2; Conserv Similarity 33.: 2; Conservative თ ہ 3 (Rel. 25, Created) 3 (Rel. 25, Last seg 1 (Rel. 40, Last ann otein from 2D-page c Periplasmic Q (Rel. (Rel. 7 9 Conservative AA 98 STANDARD; . 25, Created) .. 25, Last sequence update) L. 40, Last annotation update ----m 2D-page of plasma (Spot STANDARD; LOCATION: 2 9 1129 31, 40, PubMed=1487733; outer layer protein Chordata; Primates; 31.4%; 66.7%; 33.3%; Last sequence update) Last annotation updat Created) MW; (Serpulina hyodysenteriae). ; Brachyspiraceae; Brachyspira Periplasmic <u>, </u> Pred. No. 1.1
2; Mismatches Score 16; Pred. No. 855A19C68B4772D1 CRC64; Pred. Craniata; V Catarrhini; PRT ; PRT; Mismatches Ravier F., P., , Bjellqvist update) n flaA2 update) 1.1e+05; 2; flagellum ဖ (Spot 11) (Fragment) ھ Vertebrata; DB AA ΑA 1e+05; Hominidae; 0; (35 kDa Length Pasquali st B., proteins. Indels . V . , Indels OF hyodysenteriae
teins."; Euteleostomi; Ното sheath protein) 9; THIS UNKNOWN AROUND A COR 0 <u>,</u> 0 OF TWO CORE Gaps Gaps are 0 0 RA RA RA LMT3 B Q FT RESULT ALL7\_CA Db QY SO FT RESULT IJ Query Match Best Local S Matches 2 Query Match Best Local S Matches 2 \_CARMA Schoofs de Loof CHAIN MOD\_RES CHAIN Eur. Eukaryota; Locusta SEQUENCE CHAIN ÷ Thorpe A. Duve H., SEQUENCE SEQUENCE 7 13  $^{12}$ N ω N 6 APY :|| SPY 2 4 8

3\_LOCMI STAN LMT3\_LOCMI STAN 041489; 01-NOV-1995 (Rel. 3 01-NOV-1995 (Rel. 3 01-NOV-1995 (Rel. 3 PROTEIN IS SWISS-2DPAGE; NON\_TER NON\_TER 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Carcinustatin 7 (Contains: Carcinustatin 6; Carc Carcinus maenas (Common shore crab) (Green crab) Insecta; Pterygota; Neopt Acridomorpha; Acridoidea; NCBI\_TaxID=7004; ALL7\_CARMA STANDARD P81809; P81810; P81804; 30-MAY-2000 (Rel. 39, C TISSUE=Brain; SEQUENCE, AND SYNTHESIS TISSUE-Cerebral ganglion, and Thoracic MEDLINE-98121193; PubMed=9461295; Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus. Locustamyotropin 3 (LOM-MT-3) Neuropeptide; allatostatin "Isolation and identification of multiple NCBI\_TaxID=6759; SIMILARITY: BELONGS TO THE ALLATOSTATIN ropeptide; Amidation; Multigene family 7 IN 2 8 CARCINUSTATIN 6 IN 2 8 CARCINUSTATIN 1 IN 4 8 CARCINUSTATIN 1 IN 4 8 AMIDATION. Itostatin superfamily in the shore crab ( J. Biochem. 250:727-734(1997). FUNCTION: MAY ACT AS A NEUROTRANSMITTER LFPXTDF MFPNAPY 8 А., migratoria (Migratory locust) ta; Metazoa; Arthropoda; Mandibula ; Pterygota; Neoptera; Orthopteroi Similarity 2; Conserv Similarity Johnsen A.H., Maestro œ ە Holman IS: 4 Conservative Conservative AA; ە AA; ø P30089; STANDARD; STANDARD; 32, Created) 32, Last sequence u 32, Last annotation 825 9 1056 . 6, G.M., ITS29.48; 66.78; 31.4%; 28.6%; MW; HUMAN MW ; Hayes ΜW Acrididae; 922879CDCB4775BD CRC64; IS: <u>ب</u> 2; Mismatches 26F2B1BAF769C737 CRC64; Score 15; DB 1; Pred. No. 1.1e+05; 1; Mismatches ( Score 16; DB 1; Pred. No. 1.1e+05; PRT; PRT; J.-L., T.K., Mandibulata; 46 kDa update) Oedipodinae; Nachman update) Scott A.G., ø ganglion; æ idea; AA AA neuropeptides of Carcinus maenas. 1.67 FAMILY OR Carcinustatin Pancrustacea; R.J., Orthoptera; 0 ω .. Length NEUROMODULATOR Length Locusta Jaros Indels Indels Kochansky J.P., maenas."; 80 9 P.P., Caelifera <u>۲</u> the Hexapoda; <u>,</u> 0 ;; Gaps Gaps 0 0

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RESULT 14 SUGA\_ACHDO JD SUGA\_A AC P19991 DT 01-FEB DT 01-FEB DT 01-FEB DT 01-FEB DT 01-GT CC Insect OC Insect OC Grylli OC Grylli OC Grylli CC ACHEARY RA Wicker RT Suboef RT Su RESULT 15 ALL3\_CARM ID AC P818C DT 30-MP DT 30-MP DT 30-MP DT 30-MP DT Carci OC Eukal OC Eukal OC Malac OC Malac OC NCBI CBTC I RN [1] RP SEQUI RX MEDL RX MEDL RA DUVE B QY 많 QY Query Match Best Local S Matches 2 Matches Query Match Best Local Similarity P81806; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Carcinustatin 3. Carcinus maenas (Common shore crab) (Green crab). Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus. MCBI\_TaxID=6759; CARMA Wicker C., Wicker C.; "Isolation and structure of a peptide isolated from the subcesophageal ganglion of Acheta domesticus (orthoptera)."; Comp. Biochem. Physiol. 88C:185-187(1987). -i- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBCESOPHAGE. TISSUE=Cerebral ganglion, and Thoracic ganglion; MEDLINE=98121193; PubMed=9461295; Duve H., Johnsen A.H., Maestro J.-L., Scott A.G. ALL3\_CARMA SEQUENCE 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) SUGA\_ACHDO P19991; Neuropeptide; Amidation; Pyrokinin. MOD\_RES 9 9 ΔΜΤΓΑΡ "Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamyotropin peptide family."; Insect Biochem. Mol. Biol. 22:447-452(1992). -I- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY). -I- SIMILARITY: BELONGS TO THE PYROKININ FAMILY. InterPro; IPRO01484; Pyrokinin. Gryllidae; Gryllinae; Acheta. SEQUENCE SEQUENCE. Acheta domesticus (House cricket) Suboesophageal ganglion pentapeptide. PROSITE; PS00539; PYROKININ; SEQUENCE. NCBI\_TaxID=6997; Eukaryota; Sukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; 6 APY 8 11: 3 APF 5 Local Similarity les 2; Conserv **1 RMFPNAPYL 9** 1 RQQPFVPRL 9 GANGLIA. JS0319; ENCE 5 4; 9 AA; ; JS0319. 5 AA; 476 Conservative Conservative STANDARD; STANDARD; 1140 MW; 27.5%; 29.48; 44.48; MW ; 69D76DDDDDD00000 CRC64; AMIDATION. D5AE1772C9D776C6 CRC64; <del>ب</del> 0; Score 14; Pred. No. Score 15; Pred. No. PRT; PRT; Mismatches Mismatches Scott A.G., 1.1e+05; 7 DB 1; FROM THE SUBOESOPHAGEAL σ 1.1e+05; DB 1; AA. AA. 0,: ບາ ---Length 5; Length 9; Jaros P.P., Indels Indels 0; 0; Gaps Gaps 0; 0;

> Bp QY Query Match Best Local Similarity --+-hes 2; Conserv RT RA Allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997). -:- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR -:- SIMULTARITY: BELONGS TO THE ALLATOSTATIN FAMILY. Neuropeptide; Multigene family. SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64; Thorpe A.;. "Isolation and identification of multiple neuropeptides of the "Isolation superfamily in the shore crab Carcinus maenas."; 7 PY 8 N PΥ ω Conservative 27.5%; su 100.0%; Pr ... 0; Score 14; Pred. No. 1.
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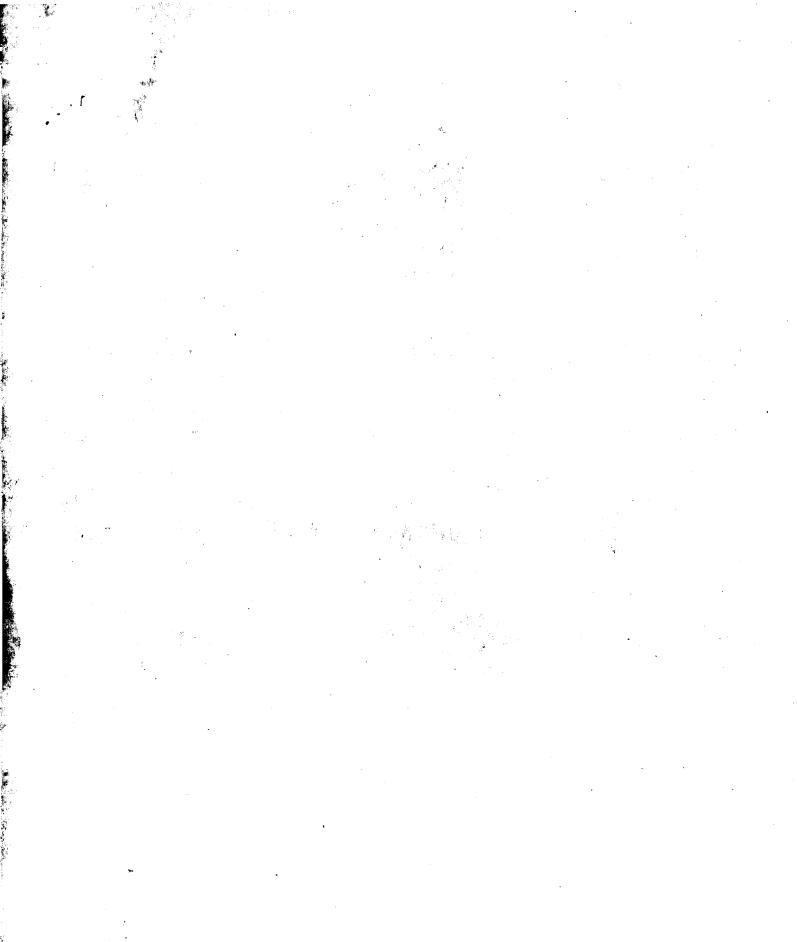
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NON_TER SEQUENCE 9.7A7; 1067 MW; Query Match Best Local Similarity 60.0% Matches 3; Conservative 4 PNAPY 8 1   1: 4 PQAPW 8 3ULT 2 09UJ50 Q9UJ50; PRELIMINARY;	<pre>RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RC TISSUE=PLACENTA; RX MEDLINE=97473511; PubMed=9332365; RA Finget L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R., RA Burrows P.D., Billips L.G.; RT "The human PD-1 gene: complete cDNA, genomic organization, and RT developmentally regulated expression in B cell progenitors."; RL Gene 197:177-187(1997). RE FMRL: U64864: AAC51774 1: -</pre>	01-MAY-2000 (TrEMBLrel. 13, Cree 01-MAY-2000 (TrEMBLrel. 13, Lasi 01-MAY-2000 (TrEMBLrel. 13, Lasi PD-1 protein (Fragment). PD-1. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Ci Mammalia; Eutheria; Primates; Ci NCBI_TaxID-9606;	SULT 1 , UMF3 PRELIMINARY; PRT; 9 AA.	13 25.5 9 16 0935G1 12 23.5 8 4 0990K3 12 23.5 8 10 P82324 12 23.5 8 11 09JLD7 12 23.5 8 11 09JLD7 13 25.5 8 11 09JLD7 14 10 10 10 10 10 10 10 10 10 10 10 10 10	13         25.5         8         5         9         2         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         099193         0991036         <	14         27.5         9         8         09T2K9         09t2k9         09t2k9         spinacia           14         27.5         9         12         067605         067605         squash           14         27.5         9         12         067605         067605         squash           14         27.5         9         12         067605         067605         squash           13         25.5         8         2         094GP4         09304P4         arthrough           13         25.5         8         2         049534         049534         049534	27.5         8         8         08WBG2         08WBg2         diadema           27.5         8         11         099940         09917         09177         anabaena           27.5         9         2         P83157         09177         anabaena           27.5         9         6         09TRU7         09tru7         bost saur           27.5         9         8         08WFS4         08wfs4         diadema           27.5         9         8         08WBX4         08wfs4         diadema           27.5         9         8         08WBX5         08w8w6         diadema           27.5         9         8         08WBX5         08w8w5         diadema	<b>t Pa</b> 14 27.5 8 8 08W8G4 08w8g4 diadema 14 27.5 8 8 08W8G3 08w8g3 diadema

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SULT 6 R7T2 Q9R7T2	Db 4 POADEL 9	SEQUENCE 9 AA; 986 Ouery Match Best Local Similarity Matches 3; Conservat	tobacco culture."; Planta 0:0-0(2000). -!- SUBCELULAR LOCATION: CELL WALL. -!- TISSUE SPECIFICITY: XYLEM. Cell wall Cell wall 9 9	<pre>RN [1] RP SEQUENCE. RC STRAIN=CV. PETIT HAVANA; RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R., RA Wojtaszek P., Bolwell G.P.; RT "Proteomic study of secondary cell wall proteins from transformed</pre>		P82429; 01-JUN-2000 01-JUN-2000 01-JUN-2000 01-JUN-2000	RESULT 5 P82429 ID P82429 PRELIMINARY; PRT; 9 AA.	QY 3 FPNAPY 8 Db 4 YPSVSY 9	Query Match '33.3%; Score 17; DB 4; Length 9; Best Local Similarity 33.3%; Pred. No. 6.7e+05; Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	DNA at chromosome 7q35."; Genomics 73:108-112(2001). EMBL; AF318295; AAK49906.1; NON_TER 1 9 9 NON_TER 9 9 SEQUENCE 9 AA; 1080 MW; 9139A2D5A77B51EA CRC64;	(1) SEQUEI MEDLII Nakaba "The l	OS Homo sapiens (Human) OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX MCBI_TaxID=9606; DM (1)]		6T

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RESULT 8 Q9TWH6	1 MLPVVP 6	2 MEDNAD 7	Query Match 31.4%; Score 16; DB 3; Length 9; Best Local Similarity 50.0%; Pred. No. 6.7e+05; Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;	mmyces lacxtis HIS4 transcriptic srences to Saccharomyces cerevis 458:72-76(1999) .38494 CAB87125.1; -	, Frei	Kluyveromyces lactis (Yeast). Kluyveromyces lactis (Yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces. NCBL_TaxID=28985; [1]	01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) HIS4 protein (Fragment).	QOPRES PRELIMINARY; PRT; 9 AA. OOPRES:	OY 7 PYL 9 Db 2 PYI 4 RESULT 7 OSPRES	Query Match31.4%; Score 16; DB 2; Length 8;Best Local Similarity66.7%; Pred. No. 6.7e+05;Matches2; Conservative1; Mismatches0; Indels0; Gaps	NON_TER 1 1 SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;	"A /18-KD DNA Sequence of Escherichia coli K-12 Genome Corresponding to the 12.7-28.0 min Region on the Linkage Map."; DNA Res. 3:137-155(1996). EMMEL: D90705; BAA35310.1; Hypothetical protein.	DJUENCE FROM N.A. NIN-K12; DLINE-97061202; PubMed-8905232; LINE-97061202; PubMed-8905232; namoto K., Inada T., Itoh T., Kajihara M., Kanai K., Hor nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Miki T., nura S., Kitagawa M., Makino K., Masuda S., Ya	Escherichia coli. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia. NGBI_TaxID=562; [1]	09R7T2; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical 1.0 kDa protein (Fragment) YOFG.	Fri Apr, 25 08:06:20 2003 us-09-625-963-1.closed.rsp
Primates; Catarrhin	Apolipoprotein A-I (Fragment). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute;	01-MAY-2000 (TrembL 01-JUN-2002 (TrembL	9UCS8 9UCS8; 1 - MAY - 2000	RESULT 10	DD 1 MSSNVP 6	Query Match 29.4%; Score 15; DB 4; Length 9; Best Local Similarity 50.0%; Pred. No. 6.7e+05; Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0	RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR EMBL; AL139188; CAC15103.1; - FT NON_TER 9 9 SQ SEQUENCE 9 AA; 951 MW; 96A3ADC772C455A5 CRC64;		in . Apiens (Human). Andrasoa: Chordata: Craniata: Vortebrata:			DY 5 NAPY 8	Query Match 29.4%; Score 15; DB 5; Length 8; Best Local Similarity 50.0%; Pred. No. 6.7e+05; Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0	<pre>RP SEQUENCE. RX MEDLINE=95323338; PubMed=7599979; RA Takabashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T., RA Fujita T., Minakata H., Nomoto K.; RT "Isolation and characterization of four novel bioactive peptides from RT a polychaete annelid, Perinereis vancaurica."; RL Comp. Biochem. Physiol. C. RL Pharmacol. Toxicol. Endocrinol. 110:297-304(1995). SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;</pre>	Periner Eukaryc Phyllod NCBI_Ta [1]		-1.closed.rspt Page

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B QY RESULT Q9S8J8 QY 998860 RESULT ₽ Matches Best Query Match Query Match Best Local Matches Fri SEQUENCE FROM N.A. MEDLINE-8612033; PubMed=3003688; Sijben-Mueller G., Hallick R.B., Alt J., West "Spinach plastid genes coding for initiation protein S11 and RNA polymerase alpha-subunit. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia. 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) Cytochrome b/f subunit IV (Fragment). 098866; 098866 Biochem. Mol. SEQUENCE 9 MEDLINE=95102521; PubMed=7804141; Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.; "Isolation and characterization of oryzatensin: a novel bioactive peptide with ileum-contracting and immunomodulating activities der Oryza sativa (Rice). Eukaryota; Viridiplantae; Streptophyta; 01-MAY-2000 (TrEMBLrel. 13, Cr 01-MAY-2000 (TrEMBLrel. 13, La 01-MAY-2000 (TrEMBLrel. 13, La 0RYZATENSIN-BIOACTIVE peptide. NCBI\_TaxID=3562; Eukaryota; Viridiplantae; Chloroplast. Spinacia oleracea SEQUENCE Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoldeae; Oryzeae; Oryza. Q9S8J8; 0928J8 from rice albumin "; NCBI\_TaxID=4530; "The apolipoprotein A-I binding protein of placenta protein of human blood are different proteins which Ehnholm C., Bozas S.E. Murphy B., Walker I.D. NON SEQUENCE SEQUENCE NON\_TER MEDLINE=92075698; 12 11 polipoprotein A-I."; 2 MFP 4 |:| 4 MYP 6 Local iochim. Apr 4 4 PNAP 7 TER PQSP 2; Conservative 2; Conserv S11 and N 5 Biophys. Acta 1086:255-260(1991). 7 ဖ PRELIMINARY; PRELIMINARY; Conservative AA; 08:06:20 AA; Biol. s 1. Int. 3 1093 MW; (Spinach). 186 S.E., Tenkanen I.D.; PubMed=1742316; 29.48; 66.78; 29.48; 50.08; ە MW; 33:1151-1158(1994). W; 0E8C67377B56877B CRC64; 2003 7FE37775A6C7776B CRC64; Last sequence update) Last annotation updat Score 15; DB Pred. No. 6.7e 1; Mismatches ;-Score 15; DB Pred. No. 6.76 1; Mismatches 1. Created) PRT; PRT; н., 15; DB 4; No. 6.7e+05; Kirszbaum 7 6.7e+05; φ Embryophyta; Tracheophyta; DB 10; Westhoff P., AA. ΑA Poales; Poaceae; factor update) 0 н ;; г., Length Length Indels Indels Metso and t ., Herrmann R.G IF-1, ribosomal , o 9 the the SP-40,40 bind to сı . 0 0; derived Gaps Gaps us-09-625-963-1.closed.rspt 0 0 RESULT P82858 QY RESULT Q07624 Dp B QY SQ FT SQ Query Match Best Local S Matches 2 Matches Query Match Best Local : P82858; Ol-MAR-2001 (TrEMBLrel. 16, Created) Ol-MAR-2001 (TrEMBLrel. 16, Last sequence up Ol-JUN-2001 (TrEMBLrel. 17, Last annotation Ol-JUN-2001 (TrEMBLrel. 17, Last annotation Uricase (EC 1.7.3.3) (Urate oxidase) (Fragme -!- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O - 5-HYDROXYISOU H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN) -!- SUBCELULAR LOCATION: PEROXISOMAL (BY SIMILARITY). -!- DEVELOPMENTAL STAGE: GERMINATION. -!- SIMILARITY: BELONGS TO THE URICASE FAMILY. Aguilar M., Montalbini F Submitted (NOV-2000) to -i- FUNCTION: INVOLVED I Puccinia recondita f. sp. triseti. Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae; Uredinales; Pucciniaceae; Puccinia. Q07624 Q07624; "Role of the open reading frames of translation and genome packaging."; EMBD J. 11:3747-3757(1992). EMBL; X67587; CAA47862.1; -. SEQUENCE FROM N.A. STRAINPRAGUE C; MEDLINE-93010967; PubMed-1327749; Donze O., Spahr P.F.; SEQUENCE, P82858 Hypothetical protein. NON\_TER 7 Rous sarcoma virus. Viruses; Retroid viruses; TISSUE=SPORE; NCBI\_TaxID=142679; SEQUENCE 01-NOV-1996 01-NOV-1998 Chloroplast. NON\_TER InterPro; NCBI\_TaxID=11886; Hypothetical protein (Fragment). 01-NOV-1996 SEQUENCE Nucleic Acids Res. 14:1029-1044(1986) EMBL; X03496; CAA27215.1; -. 14 13 |: | 4 PSIP 4 PFL 4 PNAP 7 7 PYL 9 SIMILARITY: BELO erPro; IPR002042; AND FUNGI. Similarity 2; Conserv 2 Similarity ი FUNCTION, 4 6 (TrEMBLrel. 01, 0 6 (TrEMBLrel. 01, 1 8 (TrEMBLrel. 08, 1 7 AA; 7 Montalbini P., Pineda M.; NOV-2000) to the SWISS-PROT data bank. N: INVOLVED IN HOST-PARASITE RELATIONSHIP PRELIMINARY; Conservative PRELIMINARY; Conservative AA; ш 672 MW; 907 AND 27.5%; 50.0%; 7 27.5%; 66.7%; Uricase щ MW; DEVELOPMENTAL Retroviridae; 776045A7687DD6F0 CRC64; 644729D77409C420 CRC64; Last sequence update) Last annotation update) 1. Score 14; Pred. No. Created) <u>ب</u> Score 14; DB 8; Pred. No. 6.7e+05, PRT; PRT; Mismatches Mismatches Rous (Fragment) STAGE , DB 15; . 6.7e+05; æ 2 Alpharetrovirus on update) AA sarcoma Ş , 8; 15 <u>..</u> <u>,</u> 5 - HYDROXY I SOURATE Length Length virus Indels Indels BETWEEN 7; leader RNA .... 0 0 PLANTS Gaps Gaps + ĥ Page

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s] fo	72. 97.	·	AL (e; 9 AA ) ) ) ) ) ) ) ) ) ) ) ) ) ) ) ) ) )	2221 2223 2223 2223 2223 2223 2223 2223					
INNOVATIONS LTD. WT-1 and GATA-1 epitopes, t ines for cancer immunotherapy Snglish.			LIGNMENTS ognised WT1 s tumour ger cancer; imm	AAV988754 AAU68682 AAU68853 AAG61915 AAG62086 ABG33152 ABG33152 ABG33152 AAG33325 AAY98697 AAU68796	AAU68909 AAG62142 ABG33379 AAY98583	xy98810 xy98808 xu68907 xu662140 xy98810	AAU68663 AAU68653 AAU68851 AAG62896 AAG62084	AAU68622 AAG61855 ABG33092 AAV98809 AAU68908 AAU68908 AAU682141 AAG52141 AAG3375 AAV98554 AAV98755	529
opes, their fragments otherapy -			; 771 peptide WT126-34 gene; leukaemia; immunotherapy.	WT1 derived immun Human Wilm's tumo Human WT1 immunog Human WT1 immunog Hunae WT1 immunog Mouse WT1 immunog Mouse WT1 immunog WT1 derived immun Human Wilm's tumo Human PUMP-1 pept	Wilm's tumour prot Human/mouse WT1 im Human/mouse WT1 im WT1 derived immuno	Human Wri immunoge Mouse Wri immunoge Wil related peptid Human/mouse Wri im Wri related peptid	Human Human Human	Human Wilm's tumou Human WTI immunoge Human WTI immunoge WTI related peptid Wilm's tumour prot Human/mouse WTI im Human/mouse WTI im Human/mouse WTI im	Human leukoo WT1 derived

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The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polyp WT1, (or variants of the immunogenic portion retaining the abili react with WT1 specific antisera and/or T cell lines or clones) comprising 16 consecutive amino acids (aa) or less of a native I polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response patients. The polypeptides, mimetics or polynucleotides can be inverted to a carrier/excipient in pharmaceutical compositions or with a carrier/excipient in pharmaceutical in vaccines. Pharma compositions and vaccines can be administered to human patients are useful tresponse in vaccines. Pharma compositions and vaccines can be administered to human patients are the polypertides.	Claim 4; Page 171; 193pp; English.	Novel polypeptides comprising an in polypeptide, useful for inhibiting diseases associated with WTI expre	WPI; 2000-293107/25.	Gaiger A, Cheever M;	(CORI-) CORIXA CORP. (GAIG/) GAIGER A.	30-SEP-1998; 98US-0164223. 25-MAR-1999; 99US-0276484.	30-SEP-1999; 99WO-US22819.	06-APR-2000.	WO200018795-A2.	Homo sapiens.	<pre>WT1; immunotherapy; immunogenic; m metastatic disease; mouse; human; vaccine.</pre>	WT1 derived immunogenic peptide SEQ	31-JUL-2000 (first entry)	AAY98670;	RESULT 2 AAY98670 AAY98670 standard; Peptide; 9 AA.	1 RMFPNAPYL 9           1 RMFPNAPYL 9	Query Match 100.0%; Score Best Local Similarity 100.0%; Pred. Matches 9; Conservative 0; Misr	Sequence 9 AA;	The present sequence is peptide epitope WT126-34, j expressing cells and found at residues 126-134 of is recognised by cytotoxic T lymphocytes. WT1 is al leukaemias, breast cancer, melanoma and ovarian can be used as a vaccine to stimulate the elimination, lymphocytes, of cancer cells aberrantly expressing nucleic acid encoding the peptide may also be used Alternatively, the peptide may be used in vitro to cytotoxic T lymphocytes.
The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WT1, (or variants of the immunogenic portion retaining the ability to react with WT1-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WT1 polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, mimetics or polynucleotides can be included with a carrier/excipient in pharmaceutical response) in vaccines. Pharmaceutical compositions and vaccines can be administered to manufacture compositions and vaccines can be administered to the accident to enhancer preferentially enhancing a cell response in sectific for the accident to be appreciated to man patients to be appreciated to man patients to compositions and vaccines can be accided to the accident to be appreciated to the part of the part of the polypeptide		comprising an immunogenic portion of a native WT1 l for inhibiting the development of malignant 3 with WT1 expression e.g. leukemia or cancer -									malignant disease; cancer; leukaemia; ; Wilm's tumour; immune response;	30 ID NO:185.					ore 51; DB 21; Length 9; ed. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;		e epitope WT126-34, produced by WT1 residues 126-134 of the WT1 protein, which mphocytes. WT1 is aberrantly expressed in anoma and ovarian cancer. The peptide can ate the elimination, by cytotoxic T perrantly expressing WT1. In addition, the ide may also be used in the same manner. be used in vitro to produce activated

888888888888888888888888888888888888888	PT XX XX XX	PI XX XX	PA PA	PF PR PR	XX	Y PN	os XX	KW KW	DEXX	DIX	RESULT AAY987 ID A XX	Qу Db	Qu Ma	SQ	\$88888888
The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tunnor gene product polypeptide, WT1. (or variants of the immunogenic portion retaining the ability to react with WT1-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WT1 polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, minetics or polynucleotides can be included with a carrier/excipient in pharmaceutical compositions or with a non-specific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T-cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to enhance or induce an immune response specific for wT1 or a cell expression (e.g. leukemia) or cancer (especially any to inhibit the development of malignant diseases associated with WT1 expression, e.g. leukemia) or cancer (especially acute/chronit	Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer - Claim 4; Page 186; 193pp; English.	Gaiger A, Cheever M; WPI; 2000-293107/25.	CORI-) CORIXA CORP. GAIG/) GAIGER A.	30-SEP-1999; 99WO-US22819. 30-SEP-1998; 98US-0164223. 25-MAR-1999; 99US-0276484.	6-APR-2000.	W0200018795-A2.	Mus musculus.	<pre>WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia; metastatic disease; mouse; human; Wilm's tumour; immune response; vaccine.</pre>	ų.	31-JUL-2000 (first entry)	LT 3 8778 AAY98778	1 RMFPNAPYL 9 [         1 RMFPNAPYL 9	ery Match 100.0%; Score 51; DB 21; Length 9; st Local Similarity 100.0%; Pred. No. 7.8e+05; tches <sup>.</sup> 9; Conservative 0; Mismatches 0; Indels 0; Gaps	Sequence 9 AA;	expressing WT1, useful to inhibit the development of malignant diseases associated with WT1 expression, e.g. leukemia (especially acute/chronic myeloid leukemia or acute lymphocytic leukemia) or cancer (especially breast, lung, thyroid or gastrointestinal cancer, or a melanoma). AAY98501 to AAY98811 represent polypeptide sequences, and AAA13848 to AAA13862 represent PCR primers, used in the exemplification of the present invention.

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KW Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen;	
DE Mouse Wilm's tumour protein, WT1, antigenic peptide #46. XX	Db 1 RMFPNAPYL 9
DT 16-JAN-2002 (first entry) XX	1 RMFPNAPYL
AC AAU68877; XX .	; Conservat
AAU68877 ID AAU68877 standard; Peptide; 9 AA. YY	100.0%; Score 51;
RESULT 6	SO Sequence 9 AA;
Db 1.RMFPNAPYL 9	
Query Mat Best Loca Matches	creating leukaemia and sol: c cancer vaccines in treat cancer of the large intest
Sequence 9 AA;	The present invention describes a cancer antigen containin component of Wilms' tumour suppressor gene WT1 product, or
CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL), CC myelodysplastic syndromes, myeloproliferative syndromes and cancers CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,	PT Cancer antigens based on Wilm's tumor suppressor gene WT1 product or PT peptide derivatives, for cancer vaccines in treating leukemia and solid PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer
	DR WPI; 2000-195264/17. XX
	YX XX JANA H, Oka Y;
first isolated peptide, of between 9 and 40 amino acids or a first nucleic acid, encoding the peptide, in the manufacture of a medicament	
	31-JUL-1998;
Claim	XX
PT Composition for the treatment of mesotheliona comprises specific PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic PT fragments -	РИ 10-FEB-2000.
WPI; 2001-648218/74.	
Cheev	major histocompatibility complex; leukaemia
PA (CORI-) CORIXA CORP. XX	Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine
PR 22-FEB-2000; 2000US-184070P. XX	
PF 22-FEB-2001; 2001WO-US05702. XX	XX DT 24-MAY-2000 (first entry)
PD 30-AUG-2001. XX	XX AC AAY80200;
	AAY80200 ID AAY80200 standard; Peptide; 9 AA.
OS Homo sapiens.	RESULT 4
KW Human; Wilms' tumour; Wil; pleural mesothelioma; antigen; KW leukaemia; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML; KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes; KW myeloproliferative syndrome; cancer; cytostatic. YY	OY 1 RMFPNAPYL 9 Db 1 RMFPNAPYL 9
Human Wilm's tumour protein, WT1, antigenic pept	Query Match 100.0%; Score 51; DB 21; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Sequence 9 AA;
XX AC AAU68769;	, Disenc Tuke
RESULT 5 · AAU68769 ID AAU68769 standard; Peptide; 9 AA.	N H
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RESULT 7 AAG62002 ID AAG62002 standard; Peptide; 9 AA. AC AAG62002; XX 06-JUL-2001 (first entry) DT 06-JUL-2001 (first entry) XX Human WT1 immunogenic peptide SEQ ID NO: 185. XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene; KW chromosome 11p13; zinc finger transcription factor. XX W 0200125273-A2. XX W0200125273-A2. XX W0200125273-A2. XX 04-0CT-2000; 2000WO-US27465. XX 04-0CT-1999; 99US-0157459.		<pre>KW leukaemia; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML; kW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes; xX Mus musculus. XX Mus musculus. XX 9N w0200162920-A2. XX 20-AUG-2001. 22-FEB-2001; 2001WO-US05702. XX 22-FEB-2000; 2000US-184070P. X2 CORT-) CORIXA CORP. XX CORT-) CORIXA CORP. XX Cheever MA, Gaiger A; XX PF Composition for the treatment of mesothelioma comprises specific PF peptides i.e. Wilms' tumour antigen polypeptide derived antigenic PF fragments -</pre>
<pre>pp 12-APR-2001. pr 04-OCT-2000; 2000WO-US27465. XX PR 04-OCT-1999; 99US-0157459. XX CORI-) CORIXA CORP. XX PA (CORI-) CORIXA CORP. XX WPI; 2001-328324/34. PT Polypeptide comprising part of the Wilm's Tumour gene product sequence is pr used in the diagnosis and treatment of malignant diseases e.g. leukemia pr used in the diagnosis and treatment of malignant diseases e.g. leukemia XX Claim 4; Page 200; 228pp; English. XX CC from the Wilm's tumour protein WT1 and methods for their use in treating CC malignant diseases. Peptides derived from both the murine and human WT1 CC and the protein was shown to be a zinc finger transcription factor. The</pre>	<pre>Ouery Match 100.0%; Score 51; DB 22; Length 9; Best Local Similarity 100.0%; Fred. No. 7.8e+00; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 1 RMFPNAPYL 9 Db 1 RMFPNAPYL 9 RESULT 8 AAG62110 standard; Peptide; 9 AA. XX AAG62110; DT 06-JUL-2001 (first entry) XX Mouse WT1 immunogenic peptide SEQ ID NO: 293. XX KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene; XX KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene; XX Mus musculus. XX PN W0200125273-A2.</pre>	<pre>XX pA (CORI-) CORIXA CORP. XX pI Skeiky YAW, Xu J, Cheever MA, Reed SG; XX pI Steiky YAW, Xu J, Cheever MA, Reed SG; XX pr vised in the diagnostis and treatment of malignant diseases e.g. lequence is pr used in the diagnostis and treatment of malignant diseases e.g. lequence is pr used in the diagnostis and treatment of malignant diseases e.g. lequence is pr used in the diagnostis and treatment of malignant diseases e.g. lequence is pr and cancer associated with WTI - xX Claim 4; Page 183; 228pp; English. XX The present invention describes compositions comprising peptides derived CC from the Wilm's tumour protein WT1 and methods for their use in treating CC malignant diseases. Peptides derived from both the murine and human WT1 CC and the provided. The human WT1 gene is found on chromosome 11p13, CC diagnosis and treatment of cancer and leukaemia. The present sequence is cc a polypeptide described in the exemplification of the invention. XX SQ Sequence 9 AA;</pre>

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RESU ABG3	Qy Db	Ma Ma	SQ	\$88888	PS .	X P P T T	DR XX	PI	PR PR PA PA	PR	PD XX	XX	x so xx	KW KW	DE		P X E	RESULT ABG3323			Оч Ма	Be	sõ	X888	ъ
RESULT 10 ABG33347	1 RMFPNAPYL 9             1 RMFPNAPYL 9	Query Match 100.0%; Score 51; DB 23; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 9 AA;	The invention relates to an isolated WT1 polynucleotide (I) and polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are used for treating and detecting cancer in a patient, and for stimulating an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid sequences of the invention.	Example 4; Page 194; 260pp; English.	Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for ( treating and diagnosing cancer in a patient -	Boydston J;	A, McNeill PD, Smithgall M, Moulton G, Vedvick TS:	09-OCT-2000; 2000US-0685300. 15-FEB-2001; 2001US-0785019. 24-AUG-2001; 2001US-0938864. (CORI-) CORIXA CORP. (GAIG/) GAIGER A.	2000US-0684361.	11-APR-2002. 03-OCT-2001; 2001WO-US31139.	W0200228414-A1.	Homo sapiens.	tic; immunostimulant; WT1; cancer;	Human WT1 immunogenic peptide #162.	02 (first entry)	ABG31239 STANDARD; PEPTIDE; Y AA.		· · ·		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%; Score 51; DB 22; Length 9; 100.0%; Pred. No. 7.8e+05;		immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a polypeptide described in the exemplification of the invention.	Fri Apr 25 08:06:18 2003 us-09-625-963-1.cl
US Homo sapiens. XX PN W0200194944-A2. XX	cytoto immune		or DT 18-APR-2002 (first entry)	RESULT 11 AAE17298 standard; peptide; 9 AA. XX AC AAE17298;		DY IRMEPNAPYL 9 Dh IIIIIIII Dh IRMEPNAPYL 9	Query Match 100.0%; Score 51; DB 23; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SQ Sequence 9 AA;	CC The invention relates to an isolated WT1 polynucleotide (I) and CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides CC are used for treating and detecting cancer in a patient, and for CC stimulating an immune response in patient. ABG33070-ABG33405 CC represent WT1 amino acid sequences of the invention.	PS Example 4; Page 210; 260pp; English XX	PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for PT treating and diagnosing cancer in a patient - XX	DR WPI; 2002-352217/38. XX	PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS; PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J; xx	(CORI-) COF (GAIG∕) GAJ	; 1002	PR 09-0C-1-2000; 2000US-0685830. PR 15-FEB-2001; 2000US-0785019.	03-0CT-2001;	-2002.	PN WO200228414-A1. XX	xx. Mus musculus.	<pre>KW Human; mouse; cytostatic; immunostimulant; WT1; cancer; . KW immune response.</pre>	DE Wouse WT1 immunogenic peptide #44. XX	or 15-JUL-2002 (first entry)	ID ABG33347 standard; Peptide; 9 AA. XX AC ABG33347; **	l.closed.rag Page 5

	XX	PN	x s	X K W K W	XEX		AC	RES AAY ID	Db	QY	z m o	sõ	4 C	88	188	88	88	388	383	66	888	80	88	88	388	XX	XX	PI	P	X DR	PI	PA	PR	PF	PD	
4	06-APR-2000.	W0200018795 - A2	Homo sapiens.	<pre>WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia; metastatic disease; mouse; human; Wilm's tumour; immune response; vaccine.</pre>	WT1 derived immunogenic peptide SEQ ID NO:38.	31-JUL-2000 (first entry)	AAY98523;	RESULT 12 AAY98523 ID AAY98523 standard; Peptide; 9 AA. xx	1 RMFPNAPYL 9	1 RMFPNAPYL 9	Query Match100.0%;Score 51;DB 23;Length 9;Best Local Similarity100.0%;Pred. No. 7.8e+05;Matches9;Conservative0;Mismatches0;Indels0;Gaps0;	Sequence 9 AA;	ation.	is used for A2.1 restric	ing AAPC is usef	quantifying immune response in normal, infected or treated (vaccinated) patients. Composition comprising AAPC or activated T cells produced by	nere primary T cell activation allow discovery of antigens and accessory molecules, and diagnostic applications include cell-based assays for	ion and diagnostic	population of T imphocytes under conditions suitable for the activation	specific antigen (TCA), which is useful for diagnostic purposes. AAPC is also useful for activating CTLs, by contacting AAPC with a suitable	userui for identifying within a test population of cytotoxic r lymphocytes (CTLs), CTLs specifically activated against a known T-cell	relates to methods for activation of T lymphocytes. The method is also	molecule of a single type and a protein that is processed intracellularly to produce an exogenous T cell-specific epitope. The invention also	a human leukocyte antigen, HLA (major histocompatibility complex, MHC)	a eukaryotic cell expressing an antigen presention a eukaryotic cell expressing an antigen prese	mple 17; Page 40; 75pp; English.	, анстден шотесите ана ртосети .	comprises eukaryotic cell expressing antigen presenting complex naving beta2-microglobulin, exogenous accessory molecule, human leukocyte	resenting cells for activating T lymphocytes	WPI; 2002-139667/18.	Sadelain M, Latouche J;	(SLOK ) SLOAN KETTERING. INST CANCER RES.	02-JUN-2000; 2000US-209157P.	01-JUN-2001; 2001WO-US17981.	13-DEC-2001.	

RESULT AAUG865 AC AC AC AC AC AC AC AC AC AC AC AC AC	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	PR PR PR PA PA PA PA PA PA PA PA PA
<pre>LTT 13 8622 AAU68622 standard; Peptide; 9 AA. AAU68622: 16-JAN-2002 (first entry) Human Wilm's tumour protein, WT1, antigenic peptide #17. Human; Wilms' tumour; WT1; pleural mesothelioma; antigen; leukaemia; acute myeloid leukaemia; AML; chronic myeloid deukaemia; CML; acute lymphocytic leukaemia; ALL; myelodysplastic syndromes; myeloproliferative syndrome; cancer; cytostatic. Homo sapiens. W0200162920-A2. 30-AUG-2001. 22-FEB-2001; 2001WO-US05702.</pre>	eptide, useful for inhibiting the development of malignant ses associated with WT1 expression e.g. leukemia or cancer 4; Page 149; 193pp; English. resent invention describes polypeptides (I) comprising an ogenic portion of a native Wilm's Tumour gene product polype (or variants of the immunogenic portion retaining the abilit with WT1 specific antisera and/or r-cell lines or clones) eptide. The polypeptides are useful therapeutically and to accure medicaments for enhancing/inducing an adjuvant or esponse ents. The polypeptides, mimetics or polynucleotides can be in a carrier/exclpient in paramaceutical compositions or with a pecific immune response enhancer (e.g. an adjuvant or enhan rentially enhancing a T cell response) in vaccines. Pharmace sitions and vaccines can be administered to human patients to ce or induce an immune response specific for WT1 or a cell iated with WT1 expression, e.g. leukemia (especially acute/ id leukemia or acute lymphocytic leukemia) or cancer (especially 501 to AAY98011 represent polypeptide sequences, and AAA1304 862 represent PCR primets, used in the exemplification of th nt invention. nce 9 AA; tch 10.0%; Dred. No. 7.8e+05; 8; Conservative 0; Mismatches 0; Indels 0; C RMFPNAPY 8 11111111 RMPFNAPY 8	<pre>399; 99WO-US22819. 398; 98US-0164223. 399; 99US-0276484. CORIXA CORP. AAIGER A. Cheever M; D-293107/25. Cheeving an immunogenic portion contact of co</pre>

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1 RMFPNAPY 8 ·	PS Claim 4; Page 161; 228pp; English. Qy
Query Match ; 92.2%; Score 47; DB 23; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Polypeptide comprising part of the Wilm's Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI -
Sequence 9 AA;	WPI; 2001-328324/34.
represent WT1 amino acid sequences of the invention.	Skeiky YAW, Xu J, Cheever MA, Reed SG;
polypeptide encoded by (1). The mill polypeptides and polypeptides are used for treating and detecting cancer in a patient, and for etimulation an immune reacones in patient apolypolypersize	(CORI-) CORIXA CORP.
The invention relates to an isolated WT1 polynucleotide (I) and	
Example 4; Page 171; 260pp; English.	04-OCT-2000; 2000WO-US27465.
Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient -	12-APR-2001. PT PT VY
	W0200125273-A2.
, Mossman S, Evans L, Spies AG, Boyds	Homo sapiens. PI XX
A, MCNeill PD,	Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene; XX chromosome 11p13; zinc finger transcription factor. pI
(CORI-) CORIXA CORP.	Human WT1 immunogenic peptide SEQ ID NO: 38. PA
09-OCT-2000; 2000US-0685830. 15-FEB-2001; 2001US-0785019. 24-AUG-2001; 2001US-0938864.	
2000;	1855 standard; Peptide; 9 AA. XX PR
2002.	
Homo sapiens.	1 RMFPNAPY 8 . OS
Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.	Similarity 100.0%; Pred. No. 7.8e+05; KW 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; KW
Human WT1 immunogenic peptide #15.	DE DE DE VY Match 92.2%; Score 47; DR 22; Length 9;
15-JUL-2002 (first entry)	Sequence 9 AA; DT XX
1092;	preferably humans. The present sequence is an antigenic peptide of AC the invention derived from human WT1.
ABG33092 ID ABG33092 standard; Peptide; 9 AA. XX	Leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL), ABG33 myelodysplastic syndromes, myeloproliferative syndromes and cancers ID (e.g. breast, testicular, prostate, lung and ovarian) in mammals. XX
	usering for the creating of mesociations, withins tomout, preferably pleural mesotheliona and other WT1 associated malignancies e.g.
1 RMFPNAPY 8           2 RMFPNAPY .9	CC nucleic acid, encoding the peptide, in the manufacture of a medicament Qy CC for treating or preventing mesothelioma. The peptides are antigenic CC peptides derived from the Wilms' tumour protein WT1. The composition is Db
8; Conservative 0; Mismatc	The invention relates to the use of a composition comprising at least a first isolated peptide, of between 9 and 40 amino acids or a first
altch	Claim 1; Page 209; 242pp; English.
a polypeptide described in the exemplification of the invention. Sequence 9 AA;	Composition for the treatment of mesothelioma comprises specific CC peptides i.e. Wilms' tumour antigen polypeptide derived antigenic XX fragments - SQ
and the protein was shown to be a zinc tinger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and transmission of cancer and lankagenic means the present to the diagnosis of the diagnosis are particularly useful in the	
malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13,	Cheever MA, Gaiger A; CC
The present invention describes compositions comprising peptides derived from the wilm's tumour protein WT1 and methods for their use in treating	(CORI-) CORIXA CORP.
	22-FEB-2000; 2000US-184070P.
	<b>)</b> , .
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1         1	000000 000000 000000	SUMMARIES	the number of results predicted by ch than or equal to the score of the re d by analysis of the total score dist	<pre>PUD1ISAC4_APp11Cations_A: *     (cgn2_6/ptodata/lpubpaa/US08_NEW_PUB.pep:*     (cgn2_6/ptodata/l/pubpaa/US06_NEW_PUB.pep:*     (cgn2_6/ptodata/l/pubpaa/US06_NEW_PUB.pep:*     (cgn2_6/ptodata/l/pubpaa/US07_PUBCOMB.pep:*     (cgn2_6/ptodata/l/pubpaa/US07_PUBCOMB.pep:*     (cgn2_6/ptodata/l/pubpaa/US08_PUBCOMB.pep:*     (cgn2_6/ptodata/l/pubpaa/US60_VEW_PUB.pep:*     (cgn2_6/ptodata/l/pubpaa/US60_VEW_PUB.pep:</pre>	Match 100% first 45 summaries	Match	ch: 0 ch: 9	hits satisfying chosen parameters:	301932 seqs, 80129803 residues	BLOSUM62 Gapop 10.0 , Gapext 0.5	-09-625-963-1 Rmfpnapyl 9	11 25, 2003, 06:58:40 ; Search time 15 Seco (without alignments 48.078 Million cell	ı search, using sw model	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	
Sequence 38, Appl Sequence 38, Appl Sequence 324, App Sequence 247, App Sequence 267, Appl Sequence 267, App Sequence 267, App Sequence 323, App Sequence 323, App Sequence 325, App Sequence 325, App Sequence 325, App Sequence 325, App	Sequence 185, App Sequence 293, App Sequence 293, App Sequence 293, App Sequence 293, App	Description	oy chance to have a ne result being printed, distribution.	9. pa 9. pa 9. pa 10. pa 1				29135				5 Seconds nments) n cell updates/sec		78 4.	
Qy       1 RMFPNAPYL 9         IIIIIIIII         Db       1 RMFPNAPYL 9         RESULT 2         US-10-125-635A-293         : Sequence 293, Application US/10125635A         : GENERAL INFORMATION:         : GENERAL INFORMATION:         : APPLICANT: Gaiger, Alexander         : APPLICANT: Carter, Darrick         : APPLICANT: Carter, Darrick         : APPLICANT: Carter, Martin A.	US-10-125-635A-185 Query Match 100.0%; Score 51; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 2.7e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 185 LENGTH: 9 TYPE: PRT ORGANISM: Homo sapien	FILE REFERENCE: 210121.465C7 CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 NUMBER OF SEQ ID NOS: 461	RESULT 1 US-10-125-635A-185 > Dublication NO. US2003003635A1 > Publication NO. US2003003635A1 > REVERAL INFORMATION: Garger, Alexander APPLICANT: Gaiger, Alexander APPLICANT: Smithgall, Molly D. APPLICANT: Carter, Darrick APPLICANT: Chever, Martin A. APPLICANT: Chever, Martin A. APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY	ALIGNMENTS	21 41.2 / 10 US-09-822-270-9 21 41.2 9 9 US-09-835-948-74	22 43.1 9 9 US-09-938-864-326 21.5 42.2 8 9 US-09-938-864-326	22 43.1 9 9 US-10-125-635A-326 22 43.1 9 9 US-10-125-635A-326	22 $43.1$ $8$ $10$ $05-09-863-971A-822$ $43.1$ $8$ $10$ $05-09-863-971A-8$	22 43.1 7 9 US-10-912-04-921 22 43.1 7 9 US-10-912-62-321 22 43.1 7 10 US-09-731-242A-28 22 43.1 7 10 US-09-731-242A-28	25 49.0 9 10 US-09-884-441-436 25 49.0 9 10 US-09-884-441-437 23 45.1 9 10 US-09-884-441-447 23 45.1 9 10 US-10-125-635A-322	27       28       54.9       9       US-09-938-864-114       Sequence 144, App         28       28       54.9       9       US-09-938-864-124       Sequence 144, App         28       28       54.9       9       US-09-938-864-282       Sequence 282, App         29       27       52.9       8       10       US-09-938-666-6       Sequence 282, App         30       26       51.0       8       12       IIS-10-011-436-10       Sequence 10, App1	29 56.9 9 US-10-125-635A-142 28 54.9 9 US-10-125-635A-142 28 54.9 9 US-10-125-635A-144	33 64.7 9 9 US-09-938-864-269 29 56.9 9 9 US-09-835-948-128 29 56.9 9 9 US-10-125-635A-212	13 FA 7. G G HC-DG-D38-864-08

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Query Match Best Local Similarity ...tohes 9; Conserv? Query Match Best Local Similarity Matches 9; Conservi Db QY B QY US-09-938-864-293 GRGANISM: Homo sapien
US-09-938-864-185 RESULT 3 ; ORGANISM: Mus musculus US-10-125-635A-293 RESULT SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 185 LENGTH: 9 NUMBER OF SEQ ID NOS: 461 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 293 GENERAL INFORMATION: Sequence 293, Application US/09938864 Publication No. US20030072767A1 FILE REFERENCE: 210121.465C5 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILLING DATE: 2001-08-24 APPLICANT: Evans, Lawrence AppLICANT: Spies, A. Gregory APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 APPLICANT: APPLICANT: MCNeill, Patricia D. APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 APPLICANT : APPLICANT : APPLICANT: Gaiger, NUMBER OF SEQ ID NOS: 413 APPLICANT : APPLICANT : APPLICANT : APPLICANT : APPLICANT : APPLICANT: Gaiger, APPLICANT : APPLICANT : APPLICANT : TYPE: PRT TYPE: PRT LENGTH: 9 1 RMFPNAPYL 9 1 RMFPNAPYL 9 ч 1 RMFPNAPYL 9 RMFPNAPYL 9 .⊷Mossman, Moulton, Gus Vedvick, Thomas S. Sleath, Paul R. Moulton, Gus Vedvick, Thomas S. Smithgall, Molly McNeill, Patricia D. Sleath, Paul R. Mossman, Sally Smithgall, Molly McNeill, Patricia D. Conservative Conservative Alexander Alexander Sally 100.0%; 100.0%; 100.0%; 100.0%; 0 0 Score 51; Pred. No. Score 51; Pred. No. Mismatches Mismatches N N DB 9; DB 9; .7e+05; 7e+05; 0 0 Length 9; Length 9; Indels . Indels 0; 0; Gaps Gaps 0 0;

Query Match Best Local Similarity When 9; Conserve B Ŋ ; ORGANISM: Homo sapiens US-09-872-832-46 RESULT 5 US-09-872-832-46 B QY US-10-125-635A-38 RESULT ; ORGANISM: Mus musculus US-09-938-864-293 PRIOR APPLICATION NUMBER: 60/209,157 PRIOR FILING DATE: 2000-02-06 NUMBER OF SEQ ID NOS: 49 SOFTWARE: Patentin version 3.0 SEC ID NO 46 CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 NUMBER OF SEQ ID NOS: 461 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 38 Sequence 38, Application US/10125635A Publication No. US20030039635A1 GENERAL INFORMATION: Sequence 46, Application US/09872832 Patent No. US20020131960A1 GENERAL INFORMATION: Matches Query Match SEQ ID NO 293 Best APPLICANT: Gaiger, Alexander APPLICANT: Smithgall, Molly D. APPLICANT: Carter, Darrick APPLICANT: Cheever, Martin A. APPLICANT: McNeill, Patricia D. APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 CURRENT APPLICATION NUMBER: US/09/872,832 CURRENT FILING DATE: 2001-06-01 APPLICANT: Memorial Sloan-Kettering Cancer Center TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF LENGTH: 9 TYPE: PRT FILE REFERENCE: 830002-2003. NUMBER OF SEQ ID NOS: 413 SOFTWARE: FastSEQ for Windows Version 3.0 APPLICANT : APPLICANT : TYPE: PRT LENGTH : Local Similarity nes 9; Conserv 1 RMFPNAPYL 9 1 RMFPNAPYL 9 1 RMFPNAPYL 9 1 RMEPNAPYL 9 s Evans, Lawrence Spies, A. Gregory Conservative Conservative US20030039635A1 100.0%; 100.0%; 100.0%; 0; 0 Score 51; Pred. No. Score 51; Pred. No. Mismatches Mismatches N 2.7e+05; DB 10; DB 9; .7e+05; 0 ç Length 9; Length 9; Indels Indels 0 <u>,</u> Gaps Gaps <u>,</u> 0

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B QY B QY ; ORGANISM: Homo sapien US-10-125-635A-38 US-10-125-635A-324 RESULT 8 US-09-938-864-38 US-09-938-864-38 RESULT Publication No. US20 GENERAL INFORMATION: Best Query Match Best Local : Sequence SEQ ID NO 38 GENERAL INFORMATION: Sequence 38, Ap Publication No. Matches SEQ Matches Query Match APPLICANT: APPLICANT: APPLICANT: Fri Apr 25 08:06:19 2003 CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 413 APPLICANT: APPLICANT: SOFTWARE: FastSEQ for Windows Version 3.0 EQ ID NO 324 NUMBER OF SEQ ID NOS: 461 APPLICANT: Gaiger, Alexander APPLICANT: Smithgall, Molly LENGTH: 9 TYPE: PRT APPLICANT: Gaiger, APPLICANT : SOFTWARE: FastSEQ for Windows Version 3.0 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 APPLICANT: APPLICANT : APPLICANT : APPLICANT: APPLICANT: APPLICANT : APPLICANT : ORGANISM: Homo sapien ORGANISM: Homo sapien and TYPE: TYPE: PRT LENATH: ENGTH: Local Local Similarity es 8; Conserv ຎ N **1 RMFPNAPY 8 1 RMFPNAPY 8** PRT RMFPNAPY 9 RMFPNAPY 9 324, Application US/10125635A ion No. US20030039635A1 z Similarity 8; Conserv Evans, Lawrence Spies, A. Gregory Boydston, Jeremy Cheever, Martin A. McNeill, Patricia D. Smithgall, Molly D. Carter, Darrick Moulton, Gus Vedvick, Thomas S. McNeill, Patricia D. Smithgall, Molly Application US/09938864 Vo. US20030072767A1 Mossman, Sally Sleath, Paul R. Conservative Conservative Alexander 92.2%; 100.0%; 92.2%; Score 47; 100.0%; Pred. No. Mus musculus 0 0; Score 47; Pred. No Mismatches Mismatches No. NO 2.7e+05; hes 0; DB 9; 2.7e+05; hes 0; DB 9; FOR WT1 Length 9; Length 9; Indels Indels 0 0 Gaps Gaps 0 0

; TYPE: PRT ; ORGANISM: Homo US-10-125-635A-79 B Db RESULT 10 US-10-125-635A-79 QY QY US-10-125-635A-324 US-09-938-864-324 US-09-938-864-324 RESULT 9 Query Match Best Local Similarity 100. Cohes 8; Conservative CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 413 SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 324 NUMBER OF SEQ ID NOS: 461 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 79 Sequence 79, Application US/10125635A Publication No. US20030039635A1 GENERAL INFORMATION: Matches Query Match Best Local GENERAL INFORMATION: Sequence 324, Application US/09938864 Publication No. US20030072767A1 Query Match APPLICANT: Cheever, Martin A. APPLICANT: McNeill, Patricia D. APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Evans, Lawrence APPLICANT: Spies, A. Gregory APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 APPLICANT: Gaiger, Alexander APPLICANT: Smithgall, Molly APPLICANT : APPLICANT : APPLICANT: APPLICANT : APPLICANT: Gaiger, Alexander TYPE: PRT ORGANISM: Homo sapien and Mus musculus LENGTH: LENGTH : Local Similarity hes 8; Conserv 1 MEPNAPYL 8 2 MFPNAPYL 9 2 MEPNAPYL 9 1 MFPNAPYL 8 Moulton, Gus Vedvick, Thomas S. Sleath, Paul R. Mossman, Sally Carter, Darrick Smithgall, Molly D. Smithgall, Molly McNeill, Patricia D Conservative sapien 90.2%; 100.0%; 90.2%; 100.0%; 80.4%; Score 46; ; Pred. No. 0 0 Score 46; Pred. No. Score 41; Mismatches Mismatches DB 9; DB 9; DB 2.7e+05; 2.7e+05; es 0; 9; 0 Length 9; Length Length 9; Indels Indels 9; 0 <u>,</u> Gaps Gaps

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; TYPE: PRT ; ORGANISM: Homo sapien US-09-938-864-79 망 Query Match Best Local Similarity Matches 7; Conserva QY RESULT 11 US-10-125-635A-267 ; Sequence 267, Ap QY US-09-938-864-79 ; TYPE: PRT ; ORGANISM: Mus musculus US-10-125-635A-267 많 RESULT 12 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 413 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 79 LENGTH: 9 NUMBER OF SEQ ID NOS: 461 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 267 LENGTH: 9 Query Match Best Local Similarity GENERAL INFORMATION: Sequence 79, Application VUS/09938864 Publication No. US20030072767A1 GENERAL INFORMATION: Publication No. Best Local Similarity Matches 7; Conserv Matches APPLICANT : APPLICANT : APPLICANT: Evans, Lawrence APPLICANT: Spies, A. Gregory APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 APPLICANT: Cheever, Martin A. APPLICANT: McNeill, Patricia D. APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 APPLICANT: Gaiger, Alexander APPLICANT: Smithgall, Molly APPLICANT: Carter, Darrick APPLICANT: Gaiger, Alexander APPLICANT: McNeill, Patricia APPLICANT : APPLICANT : APPLICANT: 3 FPNAPYL 9 1 FPNAPYL 7 3 FPNAPYL 9 1 FPNAPYL 7 5-1 Moulton, Gus Vedvick, Thomas S. Sleath, Paul R. Mossman, Sally McNeill, Patricia D. Smithgall, Molly Smithgall, Molly D. Application US/10125635A Conservative Conservative . 0; Conservative US20030039635A1 100.0%; 80.4%; 100.0%; 80.4%; Score 41; DB 9; 1 100.0%; Pred. No. 2.7e+05 Score 41; DB 9; I ; Pred. No. 2.7e+05; 0; Mismatches 0; 0 Pred. No. 2.7e+05; Mismatches 0; 0 Length 9; Length 9; Indels Indels Indels 0 0 0; Gaps Gaps Gaps 0 0 0 Query Match Best Local Similarity Matches 7; Conservi QY ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 323 ; LENGTH: 9 ; TYPE: PAT ; ORGANISM: Homo sapien and Mus musculus US-10-125-635A-323 Query Match Best Local Similarity Thes 7; Conserv B B QY ; TYPE: PRT ; ORGANISM: Mus musculus US-09-938-864-267 QY RESULT 14 US-10-125-635A-323 RESULT 13 US-09-938-864-267 망 SEQ ID NO 267 LENGTH: 9 GENERAL INFORMATION: Sequence 323, Application US/10125635A Publication No. US20030039635A1 GENERAL INFORMATION: Sequence 267, i Publication No APPLICANT: CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 NUMBER OF SEQ ID NOS: 461 APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 413 SOFTWARE: FastSEQ for Windows Version 3.0 APPLICANT: Gaiger, Alexander APPLICANT: APPLICANT : APPLICANT : APPLICANT: Gaiger, Alexander 1 RMEPNAP 7 ||||||| 3 RMEPNAP 9 3 FPNAPYL 9 1 FPNAPYL 7 **3 FPNAPYL** FPNAPYL 7 Sutherland, R. Alec Cheever, Martin A. McNeill, Patricia D. Carter, Darrick Vedvick, Thomas S Sleath, Paul R. Mossman, Sally Smithgall, Molly Smithgall, Molly D. Evans, Lawrence Spies, A. Gregory Moulton, Gus McNeill, Patricia Application US/09938864 p. US20030072767A1 Conservative Conservative ø 78.4%; 100.0%; 80.4%; 100.0%; 0; Mismatches Score 40; DB 9; L ; Pred. No. 2.7e+05; 0 σ Score 41; Pred. No. Mismatches DB 9; I 0. 2.7e+05; FOR WT1 FOR WT1 0 0 Length 9; Length 9; Indels Indels

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Sequence 323, Application US/09938864 Publication No. US20030072767A1 GENERAL INFORMATION: APPLICANT: Gaiger, Alexander APPLICANT: McNeill, Patricia D. APPLICANT: Mostan, Sally APPLICANT: Mostan, Sally APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465CS CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT APPLICATION NUMBER: US/09/938,864 NUMBER OF SEQ ID NOS: 413 SOFTWARE: FastSEQ for Windows Version 3.0 LENGTH: 9 CORGANISM: Homo sapien and Mus musculus US-09-938-864-323 Search completed: April 25, 2003, 07:05:57 Job time : 15 secs B QY RESULT 15 US-09-938-864-323 Query Match 78.4%; Score 40; DB 9; L Best Local Similarity 100.0%; Pred. No. 2.7e+05; Matches 7; Conservative 0; Mismatches 0; 1 RMEPNAP 7 |||||| 3 RMEPNAP 9 0; Indels Length 9; 0 ; Gaps 0,;

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$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	SUMMARIES Result Query No. Score Match Length DB ID Description	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	<pre>Database : Issued_Patents_AA:* 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* 4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* 5: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*</pre>	Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	mber of hits sinner hits si	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 262574 seqs, 29422922 residues	Title: US-09-625-963-1 Perfect score: 51 Sequence: 1 RMFPNAPYL 9	1 25, 200	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 2003 Compugen Ltd. OM protein - protein search, using sw model	Fri Apr 25 08:06:20 2003
CUMPRY: U.S. CONFRY: 0.2173 COMPUTER READABLE FORM: MEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compa	GORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington	APPLICAMY: Darveau, Andre TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilms' Tumor Gene NUMBER OF SEQUENCES: 8	Glaser, T Glaser, T Ito, Cary Buckler, <i>i</i> Pelletier Haber, Dau Rose, Elli Housman, T	5 pplication US/0810 26288 RMATION: RMATION:	ALIGNMENTS	35       68.6       380       3       US-09-150-141-9       Sequence 9,         35       68.6       380       4       US-09-374-493-9       Sequence 9,         35       68.6       380       4       US-09-374-824-9       Sequence 9,         35       68.6       380       4       US-09-374-824-9       Sequence 9,	36         70.6         618         4         US-09-617-653A-8         Sequence 2         Appl           36         70.6         618         4         US-09-669-023-29         Sequence 2, Appl           36         70.6         618         4         US-09-617-653A-8         Sequence 2, Appl           36         70.6         618         4         US-09-1089-023-29         Sequence 2, Appl           36         70.6         618         5         PCT-US96-12860-2         Sequence 2, Appl           37         6.8         5         PCT-US96-12860-2         Sequence 2, Appl	36         70.6         438         5         PCT-US95-05922A-2         Sequence 2, Appl           36         70.6         618         2         US-08-511-485-8         Sequence 8, Appl           36         70.6         618         2         US-09-212-971-8         Sequence 8, Appl           36         70.6         618         4         US-09-212-971-8         Sequence 8, Appl           36         70.6         618         4         US-08-800-929A-8         Sequence 8, Appl           36         70.6         618         4         US-08-710-7         Sequence 3, Appl	701010	us-09-625-963-1.open.rai Page 1

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RESULT 3 US-08-234-783-2 Sequence 2, Application US/08234783 Patent No. 5622835 GENERAL INFORMATION: APPLICANT: Herlyn, Meenhard APPLICANT: Rouscher III, Frank J. APPLICANT: Rouscher III, Frank J. TITLE OF INVENTION: US Therefor NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSEE: Howson and Howson STAFE: Spring House Corporate Cntr, PO Box 457 CITY: Spring House CONTRY: USA SIDE 19477	Query Match 100.0%; Score 51; DB 4; Length 154; Best Local Similarity 100.0%; Pred. No. 0.04; Matches 9; Conservative 0; Mismatches 0; Indels 0; G / 1 RMFPNAPYL 9           b 40 RMFPNAPYL 48	PRIOR FILING DATE: 1989-11-13 PRIOR APPLICATION NUMBER: US 07/795,323 PRIOR FILING DATE: 1994-09-27 NUMMER OF SEQ ID NOS: 21 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 5 EQ ID NO 5 ED ID NO 5	EFERENCE: 0050.1312-011 T APPLICATION NUMBER: US/09, TF FLING DATE: 1998-03-09 APPLICATION NUMBER: US 08/10 FPLING DATE: 1993-08-02 APPLICATION NUMBER: US 07/6: FILING DATE: 1990-11-13 FILING DATE: 1990-11-13 APPLICATION NUMBER: US 07/4:	APPLICANT: Ito, Caryn Y. APPLICANT: Buckler, Alan J. APPLICANT: Pelletier, Jerry APPLICANT: Haber, Daniel A. APPLICANT: Housman, David E. APPLICANT: Housman, David E. APPLICANT: Bruening, Wendy APPLICANT: Bruening, Wendy APPLICANT: Bruening, Wendy TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilms' Tumor Gene	SULT 2 -09-037-179B-5 Sequence 5, Application US/09037179B Patent No. 6316599 GENERAL INFORMATION: APPLICANT: Glaser, Thomas M.	1 RMFPNAPYL 9           40 RMFPNAPYL 48	Query Match 100.0%; Score 51; DB 1; Length 154; Best Local Similarity 100.0%; Pred. No. 0.04; Matches 9; Conservative 0; Mismatches 0; Indels 0; G
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APPLICATION: 435 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: US 08/234,783 APPLICATION NUMBER: US 08/234,783 PILING DATE: 28-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215 REFERENCE/DOCKET NUMBER: WST48AUSA TELECOMMUNICATION INFORMATION: TELEPHONE: 215-540-9200 RESULT 4 US-08-456-907-2 B QY ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-234-783-2 Sequence 2, Application US/08456907 Patent No. 5633142 Query Match 100.0%; Score 51; DB 1; Best Local Similarity 100.0%; Pred. No. 0.055; Matches 9; Conservative 0; Mismatches TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: ATCOASSIFICATION: 435 ATCORNEY/AGENT INFORMATION: NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215 REFERENCE/DOCKET NUMBER: WST4 TELECOMMUNICATION INFORMATION: TELEPHONE: 215.540-9200 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC competible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0; Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/456,907 APPLICANT: Morris, Jennifer APPLICANT: Rauscher III, Frank J. APPLICANT: Rodeck, Ulrich TITLE OF INVENTION: WT1 Monoclonal Antibodies and TITLE OF INVENTION: Use Therefor SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS: ADDRESSEE: Howson and Howson SEQUENCE CHARACTERISTICS: APPLICANT: COMPUTER READABLE FORM: MEDIUM TYPE: IBM FC compatible OPERATING SYSTEM: PC-DOS/MS-DOS NUMBER OF SEQUENCES: ||||||||| 137 RMFPNAPYL 145 ZIP: COUNTRY : STREET: Spring House Corporate Cntr, PO Box 457 CITY: Spring House STATE: Pennsylvania LENGTH: 210 amino acids TYPE: amino acid TOPOLOGY: linear FILING DATE: 1 RMFPNAPYL 9 APPLICATION NUMBER: 19477 USA Herlyn, Meenhard US/08/234,783 N ... WST48USA DB 1; Length 210; <u>,</u> Indels Methods of .... 0 Gaps

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RESULT 6 US-08-102-942A-2 뭥 QY QY Query Match Best Local Similarity Worknes 9; Conserve ; MOLECULE TYPE: protein US-08-456-907-2 Db RESULT 5 ; MOLECULE TYPE: protein PCT-US95-05523-2 PCT-US95-05523-2 Sequence 2, Application US/08102942A Patent No. 5726288 Query Match Best Local GENERAL INFORMATION Matches GENERAL INFORMATION: TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO: 2: APPLICANT: SEQUENCE CHARACTERISTICS: TELEPHONE: 215-540-9200 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS TITLE OF INVENTION: TITLE OF INVENTION: PRIOR APPLICATION DATA: FILING DATE: 28-APR-1994 ATTORNEY/AGENT INFORMATION: APPLICANT: NUMBER OF SEQUENCES: 137 RMFPNAPYL 145 137 RMFPNAPYL 145 TELEPHONE: 215-540-5818 TOPOLOGY : TYPE: REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Local Similarity es 9; Conserv NAME : APPLICATION NUMBER: US 08/234,783 CLASSIFICATION: FILING DATE: COUNTRY : CITY: TOPOLOGY : LENGTH: STATE: STREET : TYPE: 1 RMFPNAPYL 9 APPLICATION NUMBER: ADDRESSEE : **1 RMFPNAPYL 9** ENGTH: Ę 19477 i: 210 amino acids amino acid Bak, Mary E. Spring House amino acid Application PC/TUS9505523 Pennsylvania The Wistar Institute of Anatomy and Biology NVENTION: WT1 Monoclonal Antibodies and NVENTION: Methods of Use Therefor 210 amino acids Spring House Corporate Cntr, PO Box 457 Call, Katherine M. Glaser, Thomas M. Conservative USA Conservative linear linear Howson and Howson 100.0%; 100.0%; 31,215 PCT/US95/05523 <u>,</u> 0 WST48PCT Score 51; DB 5; Pred. No. 0.055; Score 51; DB 1; Pred. No. 0.055; Mismatches Mismatches DB 1; 0; 0; Length 210; Length 210; Indels Indels 0 0 Gaps Gaps 0,; 0;

B Ŷ RESULT 7 US-09-037-179B-2 US-08-102-942A-2 Matches GENERAL Sequence 2, Application US/09037179B Patent No. 6316599 Query Match Best Local : APPLICANT: Haber, Daniel A. APPLICANT: Rose, Elise A. APPLICANT: Housman, David E. APPLICANT: Bruening, Wendy APPLICANT: Bruening, Wendy APPLICANT: Darveau, Andre TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilms' Tumor Gene FILE REFERENCE: 0050.1312-011 CURRENT APPLICATION NUMBER: US/09/037,179B CURRENT FILING DATE: 1998-03-09 ENERAL INFORMATION: APPLICANT: Call, Katherine M. APPLICANT: Glaser, Thomas M. APPLICANT : APPLICANT : APPLICANT : PRIOR FILING DATE: PRIOR APPLICATION NUMBER: US 08/102,942 INFORMATION FOR SEQ ID NO: TOPOLOGY: linear MOLECULE TYPE: protein APPLICANT: APPLICANT: SEQUENCE CHARACTERISTICS: LENGTH: 345 amino acids CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA: COMPUTER READABLE FORM: TITLE OF INVENTION: Localization and Characterization TITLE OF INVENTION: Wilms' Tumor Gene CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: APPLICANT : APPLICANT : APPLICANT : 42 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 Loca l TYPE : NAME: Granahan, Pat. REGISTRATION NUMBER: APPLICATION NUMBER: US/08/102,942A FILING DATE: 02-AUG-1993 TELEFAX : TELEPHONE : REFERENCE/DOCKET NUMBER: ZIP: STATE : CITY: Lexington 1 RMFPNAPYL 9 MEDIUM TYPE: COUNTRY : STREET : ADDRESSEE : RMFPNAPYL 50 02173 Similarity 9; Conserv amino acid Massachusetts (: U.S. Ito, Caryn Y. Buckler, Alan J. Pelletier, Jerry Two Militia Drive 617-861-9540 Conservative Pelletier, Jerry Haber, Daniel A. Rose, Elise A. Darveau, Andre Bruening, Wendy Housman, David E. Buckler, Alan J. Ito, Caryn Hamilton, Brook, Smith & Reynolds, P.C 617-861-6240 Floppy disk 1993-08-02 Patricia 100.0%; 100.0%; ۲. 32,227 <u>າ</u> <u>,</u> MIT-5194A2 Score 51; DB 1; Pred. No. 0.093; DB 1; Length 345; Indels of the 0 Gaps 0

Page w 뭥 Q 망 QY ; MOLECULE TYPE: protein US-08-234-783-4 US-09-037-179B-2 RESULT SOFTWARE: F Best Local Similarity Matches 🖕 9; Conserv Query Match Sequence 4, Query Match Best Local : Matches 08-234-783-4 NUMBER OF SEQ ID NOS: GENERAL INFORMATION: PRIOR FILING DATE: PRIOR APPLICATION NUMBER: US 07/614,161 PRIOR FILING DATE: 1990-11-13 TYPE: PRT ORGANISM: Homo sapien INFORMATION FOR SEQ ID NO: Lent No. COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA: LENGTH : ATTORNEY/AGENT INFORMATION: NAME: Bak, Mary E. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk SEQUENCE CHARACTERISTICS: TELECOMMUNICATION INFORMATION: CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES: TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of TITLE OF INVENTION: Use Therefor APPLICANT : APPLICANT : **NPPLICANT**: PPLICANT : **126 RMFPNAPYL 134** TYPE: amino acid STREET : Local Similarity les 9; Conserv **TOPOLOGY**: **TELEFAX**: TELEPHONE : REFERENCE/DOCKET NUMBER : **REGISTRATION NUMBER:** CLASSIFICATION: FILING DATE: APPLICATION NUMBER: ZIP: COUNTRY : STATE : CITY: **42 RMFPNAPYL 50** LENGTH : ADDRESSEE : 1 RMFPNAPYL 9 **1 RMFPNAPYL 9** APPLICATION NUMBER: US 07/795,323 FILING DATE: 1989-11-13 APPLICATION NUMBER: US 07/435,780 345 FastSEQ 19477 Spring House 5622835 Application US/08234783 Pennsylvania 429 amino acids Spring House Corporate Cntr, : 215-540-9200 215-540-5818 Conservative USA Rodeck, Ulrich Rauscher III, Morris, Jennifer Herlyn, Meenhard Conservative linear Howson and Howson for Windows Version 4.0 1994-09-27 435 100.0%; 100.0%; 100.0%; Score 51; DB 4; Length 345; 100.0%; Pred. No. 0.093; US/08/234,783 31,215 4: Frank J. WST48USA 0 0 Score 51; Pred. No. Mismatches Mismatches PO Box 457 0.12; DB 1; 0 0 . 25 Length 429; Indels Indels 0 <u>,</u> Gaps Gaps <u>,</u> 0

Dp QY RESULT 9 US-08-456-907-4 PCT-US95-05523-4 RESULT 10 ; MOLECULE TYPE: US-08-456-907-4 Query Match Best Local S Matches 9 Sequence 4, Application PC/TUS9505523 GENERAL INFORMATION: Sequence 4, App... Sequence 4, App... GENERAL INFORMATION: TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO: TYPE: amino acids TOPOLOGY: lin OLECHIE PRIOR APPLICATION 135 PRIOR APPLICATION DATA: APPLICANT: The Wist TITLE OF INVENTION: TITLE OF INVENTION: TELEPHONE: 215-540-9200 SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: US 0: FILING DATE: 28-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: Bak, Mary E. SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: CORRESPONDENCE ADDRESS COMPUTER READABLE FORM: CORRESPONDENCE ADDRESS : NUMBER OF SEQUENCES: NUMBER OF SEQUENCES: TITLE OF INVENTION: WT1 Monoclon TITLE OF INVENTION: Use Therefor APPLICANT: APPLICANT : APPLICANT : APPLICANT : 126 RMFPNAPYL 134 Local Similarity nes 9; Conserv ZIP: STREET : COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS MEDIUM TYPE: COUNTRY : STATE : CITY: REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER: FILING DATE: APPLICATION NUMBER: COUNTRY : STATE: CITY: STREET : ZIP: ADDRESSEE: Howson and Howson ADDRESSEE : 1 RMFPNAPYL 9 19477 SSEE: Howson and Howson T: Spring House Corporate Cntr, Spring House : Pennsylvania 19477 Spring House Pennsylvania Application US/08456907 Spring House Corporate Cntr, PO Box 457 USA The Wistar Institute of Anatomy and Biology VENTION: WT1 Monoclonal Antibodies and USA Rodeck, Ulrich Conservative Rauscher III, Frank J. Morris, Jennifer Herlyn, Floppy disk Methods of Use Meenhard 100.0%; Score 51; 100.0%; Pred. No. WT1 Monoclonal Antibodies and Methods US/08/456,907 31,215 4: 08/234,783 <u>,</u> WST48AUSA Mismatches Theretor 0.12; Po DB 1; Box 457 0 Length 429 Indels 0 H <u>,</u> Gaps

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Q RESULT 11 US-08-102-942A-4 ; MOLECULE TYPE: protein PCT-US95-05523-4 Patent No. 57 Sequence Matches Query Match Best Local S TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO: 4: GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: COMPUTER READABLE FORM: MEDLUM TYPE: FLOPPY disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C STREET: Two Militia Drive TITLE OF SEQUENCE CHARACTERISTICS: LENGTH: 429 amino acids TYPE: amino acid FILING DATE: 28-APR-1994 ATTORNEY/AGENT INFORMATION: CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: APPLICANT : APPLICANT : APPLICANT : APPLICANT : APPLICANT : TELECOMMUNICATION INFORMATION: TELEPHONE: 215-540-9200 CURRENT APPLICATION DATA: APPLICANT : APPLICANT: PRIOR APPLICATION DATA: 126 RMFPNAPYL 134 APPLICATION NUMBER: US/0 FILING DATE: 02-AUG-1993 CLASSIFICATION: 530 TELEPHONE: 215-540-5818 2 I P : COUNTRY : STATE : TOPOLOGY : APPLICATION NUMBER: PCT/US95/05523 FILING DATE: NAME : NAME : APPLICATION NUMBER: US 08/234,783 FILING DATE: 28-APR-1994 CLASSIFICATION: SOFTWARE : REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER: WST48PCT REGISTRATION NUMBER: OPERATING SYSTEM: COMPUTER: REFERENCE/DOCKET 1 RMFPNAPYL 9 MEDIUM TYPE: ÿ Similarity 9; Conserv 02173 Lexington Granahan, Patricia INVENTION: INVENTION: Bak, Mary E. Massachusetts Application US/08102942A U.S. 100.0%; ilarity 100.0%; Conservative C Darveau, Andre Glaser, Thomas M. Bruening, Wendy ROSe, Pelletier, Jerry Haber, Daniel A. Buckler, Alan J. Ito, Rose, Elise A. Housman, David E. Call, linear PatentIn Release #1.0, Version #1.25 E: Floppy disk IBM PC compatible Caryn Y. Katherine NUMBER: Localization and Characterization of the Wilms' Tumor Gene PC-DOS/MS-DOS œ US/08/102,942A 31,215 32,227 0 ;; MIT-5194A2 Score 51; DB 5 Pred. No. 0.12; Mismatches DB 5; <u>,</u> Length 429; Indels 0 Gaps 0 RESULT 12 US-08-102-942A-6 밇 QУ US-08-102-942A-6 US-08-102-942A-4 Best Local Similarity Matches 9; Conserv Query Match Sequence 6, Application US/08102942A Patent No. 5726288 Matches Best Query Match GENERAL INFORMATION: TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 449 amino acids TOPOLOGY: 1 MOLECULE TYPE: TELEPHONE: 617-861-6240 ATTORNEY/AGENT INFORMATION: CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MOLECULE TYPE: protein SEQUENCE CHARACTERISTICS: LENGTH: 449 amino acid CORRESPONDENCE ADDRESS: TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilms' Tumor Gene APPLICANT : TELECOMMUNICATION INFORMATION: NUMBER OF SEQUENCES: APPLICANT : APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT : APPLICANT : APPLICANT : APPLICANT : 126 RMFPNAPYL 134 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, STRANDEDNESS : CLASSIFICATION: APPLICATION NUMBER: US/0 FILING DATE: 02-AUG-1993 Local Similarity les 9; Conserv TYPE: TELEPHONE : REFERENCE/DOCKET NUMBER : **REGISTRATION NUMBER:** MEDIUM TYPE: ZIP: COUNTRY : STATE : CITY: Lexington STREET : TOPOLOGY : TYPE: NAME : ADDRESSEE : 1 RMFPNAPYL 9 TELEPHONE: 02173 amino acid amino acid Granahan, Massachusetts Two Militia Drive 449 amino acids Pelletier, Jerry Haber, Daniel A. Rose, Elise A. Housman, David E. 100.0%; ilarity 100.0%; Conservative C U.S. : 617-861-6240 617-861-9540 Glaser, Thomas M. Conservative Darveau, Andre Bruening, Wendy Ito, Caryn Y. Buckler, Alan J. Call, linear linear Hamilton, Brook, Smith & Reynolds, P.C. Floppy disk protein not relevant Katherine M. Patricia 530 100.0%; US/08/102,942A 32,227 6: 4 : MIT-5194A2 <u>,</u> <u>,</u> Score 51; DB 1 Pred. No. 0.12; Score 51; Pred. No. Mismatches Mismatches Version #1.30 0 DB 1; Length 449; DB 1; Length 449; 12; 0 ; 0

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SOFTWARE: 1 SEQ ID NO 6 PRIOR PRIOR NUMBER OF SEQ ID NOS: PRIOR APPLICATION NUMBER: US 07/435,780 PRIOR FILING DATE: 1989-11-13 PRIOR APPLICATION NUMBER: US 07/795,323 PRIOR FILING DATE: 1994-09-27 PRIOR PRIOR LENGTH: 449 APPLICATION NUMBER: US 08/102,942 FILING DATE: 1993-08-02 APPLICATION NUMBER: US 07/614,161 FILING DATE: 1990\_11113 FastSEQ for Windows Version 4.0 21 Page ი

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Q 뭥 çy Ъ US-09-037-179B-6 ; OTHER INFORMATION: Murine US-09-037-179B-4 US-09-037-179B-4 RESULT 13 RESULT 14 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 Sequence 4, Application US/09037179B Patent No. 6316599 Sequence 6, Application US/09037179B Patent No. 6316599 Matches Query Match GENERAL Best Local Similarity Matches 9; Conserv GENERAL APPLICANT: APPLICANT: CURRENT APPLICATION NUMBER: US/09/037,179B CURRENT FILING DATE: 1998-03-09 PRIOR APPLICATION NUMBER: US 08/102,942 PRIOR FILING DATE: 1993-08-02 PRIOR APPLICATION NUMBER: US 07/614,161 PRIOR FILING DATE: 1990-11-13 PRIOR FILING DATE: 1989-11-13 PRIOR FILING DATE: 1989-11-13 APPLICANT: Bruening, Wendy APPLICANT: Darveau, Andre TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilms' Tumor Gene FILE REFERENCE: 0050.1312-011 FILE REFERENCE: 0050.1312-011 APPLICANT: Call, Katherine M. APPLICANT: Glaser, Thomas M. APPLICANT: Ito, Caryn Y. APPLICANT: Bruening, Wendy APPLICANT: Darveau, Andre TITLE OF INVENTION: Localization and Characterization of TITLE OF INVENTION: Wilms' Tumor Gene FILE REFERENCE: 0050.1312-011 CURRENT APPLICATION NUMBER: US/09/037,179B CURRENT FILIANG DATE: 1998-03-09 APPLICANT: Call, Katherine M. APPLICANT: Glaser, Thomas M. APPLICANT: Ito, Caryn Y. PRIOR APPLICATION NUMBER: US 07/795,323 PRIOR FILING DATE: 1994-09-27 APPLICANT : APPLICANT : APPLICANT: APPLICANT : NUMBER OF SEQ ID NOS: APPLICANT: APPLICANT : APPLICANT : APPLICANT : ORGANISM: Unknown FEATURE: TYPE: PRT ENGTH: 126 RMFPNAPYL 134 1 RMFPNAPYL 9 ||||||||| 126 RMFPNAPYL 134 1 RMFPNAPYL 9 INFORMATION: INFORMATION: 449 Pelletier, Jerry Haber, Daniel A. Rose, Elise A. Ito, Caryn Y. Buckler, Alan J. Pelletier, Jerry Haber, Daniel A. Housman, David E. Housman, David E. Buckler, Alan J. Rose, Elise A. Conservative 100.0%; 100.0%; 0 Pred. No. Score 51; Mismatches 0.12; DB 4; Length 449; 0 Indels the <u>,</u> Gaps 0 QY US-08-975-080-26 RESULT 15 US-08-975-080-26 B ; ORGANISM: Homo sapien US-09-037-179B-6 Query Match Best Local Similarity Matches 6; Conserv Patent No. Sequence 26, Application US/08975080 Patent No. 6245523 Matches Query Match Best TELEFAX: 202-467-7176 INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: TYPE: PRT COMPUTER: IIM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/0 FILING DATE: 20-NOV-1997 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Altieri, TITLE OF INVENTION: TITLE OF INVENTION: SEQUENCE CHARACTERISTICS: LENGTH: 50 amino acids ATTORNEY/AGENT INFORMATION: NAME: Adler, Reid G. REGISTRATION NUMBER: 30,988 MOLECULE TYPE: TELEPHONE: 202-467-7000 STREET: 1000 CITY: Washington CORRESPONDENCE ADDRESS : NUMBER OF SEQUENCES: 126 RMFPNAPYL 134 TOPOLOGY : STRANDEDNESS : APPLICATION NUMBER: FILING DATE: 20-NO ZIP: COUNTRY : Local Similarity les 9; Conserv TYPE: REFERENCE/DOCKET NUMBER: 1 RMFPNAPYL 9 ADDRESSEE : 20036-5869 amino acid 50 amino acids E: MORGAN, LEWIS & BOCKIUS LLP 1800 M Street, N.W. USA Conservative Conservative Linear protein 20-NOV-1996 100.08; 100.08; 72.5%; 66.7%; SURVIVIN, A PROTEIN THAT INHIBITS CELLULAR APOPTOSIS, AND ITS MODUL Darío C. SURVIVIN, ω 5 US 60/031,435 US/08/975,080 26: 0; 1; Mismatches Score 37; I Pred. No. 3 044574-5022-01-WO Score 51; DB 4 Pred. No. 0.12; Mismatches

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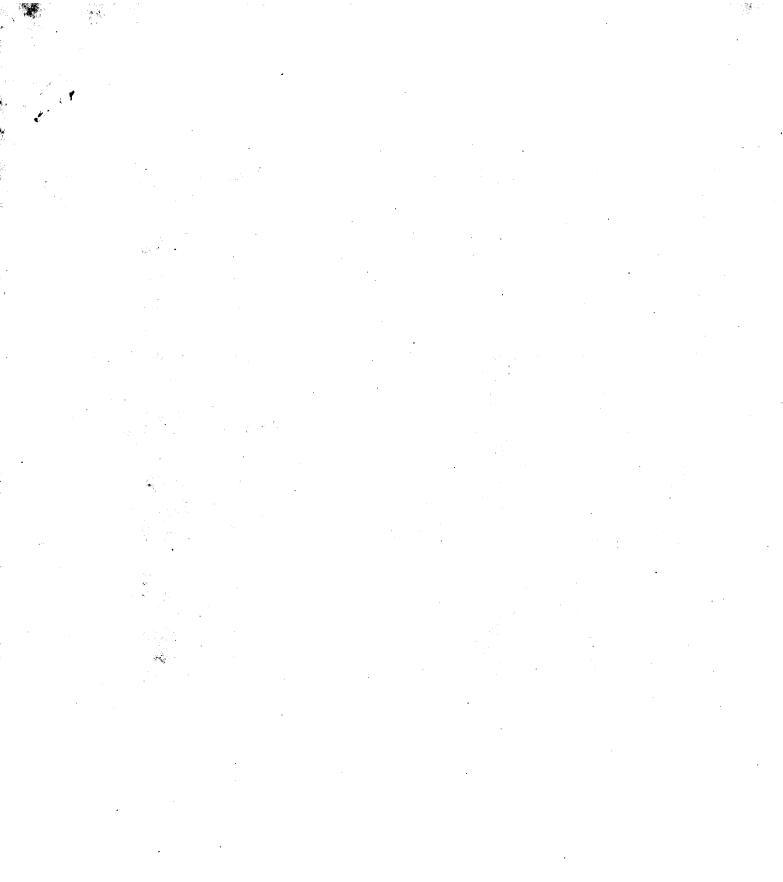
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	51 100.0 344 9 US-10-125-635A-391 Sequence 35
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	51 100.0 344 9 US-10-123-633A-391 Sequence 51 100.0 344 9 US-09-938-864-391 Sequence 51 100.0 345 10 US-09-929-315-2 Sequenc 51 100.0 345 10 US-09-993-215-2 Sequenc
OM protein - protein search, using sw model	51 100.0 362 9 US-10-125-635A-394 Sequence 51 100.0 362 9 US-09-938-864-394 Sequence
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Title: US-09-625-963-1 Perfect score: 51 Sequence: 1 RMFPNAPYL 9	51 100.0 420 9 US-09-938-864-393 Sequence 51 100.0 428 9 US-10-125-635A-405 Sequence 51 100.0 428 9 US-10-125-635A-405 Sequence
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	51 100.0 429 9 US-10-125-635A-408 Sequence 51 100.0 429 9 US-0938-864-408 Sequence 51 100.0 449 9 US-10-125-635A-319 Sequence
Searched: 301932 seqs, 80129803 residues	51 100.0 449 9 US-10-125-635A-404 Sequence 51 100.0 449 9 US-10-125-635A-404 Sequence
Total number of hits satisfying chosen parameters: 301932	51 100.0 449 9 US-09-938-864-320 Sequence 51 100.0 449 9 US-09-938-864-320 Sequence
Minimum DB seq length: 0 Maximum DB seq length: 200000000	51 100.0 449 10 US-09-929-315-4 Sequence 51 100.0 449 10 US-09-929-315-6 Sequence 51 100.0 449 10 US-09-929-315-6 Sequence
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Sequence
Database : Published_Applications_AA:* 1	RESULT 1 US-10-125-635A-185 Sequence 185, Application US/10125635A Publication No. US20030039635A1 GENERAL INFORMATION: APPLICANT: Gaiger, Alaxander APPLICANT: Gaiger, Alaxander APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Cheever, Martin A. APPLICANT: Cheever, Martin A. APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printe and is derived by analysis of the total score distribution.	; FILE REFERENCE; 210121.465C7 ; CURRENT APPLICATION NUMBER: US/10/125,635A ; CURRENT FILING DATE: 2002-07-19 ; NUMBER OF SEQ ID NOS: 461 ; SOFTWARE: FastSEQ for Windows Version 3.0
Score Match Length DB ID	
51 100.0 9 9 US-10-125-635A-185 51 100.0 9 9 US-10-125-635A-293 51 100.0 9 9 US-09-938-864-185 . 51 100.0 9 9 US-09-938-864-185 . 51 100.0 9 9 US-09-938-864-293	
51 100.0 23 9 US-10-125-633A-2 51 100.0 23 9 US-10-125-635A-3 51 100.0 23 9 US-10-125-635A-3 51 100.0 23 9 US-09-938-864-2 51 100.0 23 9 US-09-938-864-2	OP     OP     I       11     Qy     1       11     Db     1       11     Db     1       11     Db     1       11     NMEPNAPYL     9
10         51         100.0         152         9         US-10-125-635A-343         Sequence 343         App           11         51         100.0         152         9         US-10-125-635A-343         Sequence 343         App           12         51         100.0         152         9         US-09-938-864-343         Sequence 343         App           13         51         100.0         154         10         US-09-993-215-5         Sequence 5, Appli           13         51         100.0         154         10         US-09-993-215-5         Sequence 5, Appli           14         51         100.0         214         9         US-10-125-635A-395         Sequence 345, App	· · · · UR
51 100.0 214 9 US-09-938-864-395 51 100.0 256 9 US-10-125-633A-335 51 100.0 256 9 US-10-125-633A-335 51 100.0 256 9 US-10-125-635A-461 51 100.0 280 9 US-10-125-635A-461	pp ; GENERAL INFORMATION: pp ; APPLICANT: Gaiger, Alexander pp ; APPLICANT: Gaiger, Alexander pp ; APPLICANT: Carter, Darrick pp ; APPLICANT: Carter, Darrick

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Query Match Best Local Similarity Motohes 9; Conserv? 망 QY Ş ; TYPE: PRT ; ORGANISM: Mus musculus US-10-125-635A-293 ; ORGANISM: Homo sapien US-09-938-864-185 US-09-938-864-185 昂 US-09-938-864-293 RESULT 4 RESULT Query Match Best Local Similarity Thes 9; Conserv SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 185 LENGTH: 9 NUMBER OF SEC ID NOS: 461 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 293 LENGTH: 9 GENERAL Publication No. GENERAL Sequence 185, Publication No. APPLICANT: Gaiger, Alexander APPLICANT: McNeill, Patricia D. APPLICANT : APPLICANT : CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-0 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 APPLICANT : NUMBER OF SEQ ID NOS: 413 APPLICANT: APPLICANT : APPLICANT : APPLICANT : APPLICANT: Gaiger, Alexander FILE REFERENCE: 210121.465C7 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY APPLICANT APPLICANT : APPLICANT: MCNeill, Patricia D APPLICANT TYPE: PRT **NPPLICANT**: **APPLICANT**: **NPPLICANT: NPPLICANT**: -**1 RMFPNAPYL 9** 1 RMFPNAPYL 9 RMFPNAPYL 9 RMFPNAPYL 9 INFORMATION: INFORMATION: Moulton, Gus Vedvick, Thomas S Smithgall, Molly Moulton, Gus Vedvick, Thomas S. Sleath, Paul R. Mossman, Sally Evans, Lawrence Spies, A. Gregory Boydston, Jeremy Sleath, Paul R Mossman, Sally Smithgall, Molly McNeill, Patricia D. Sutherland, Application US/09938864 0. US20030072767A1 Application US/09938864 D. US20030072767A1 Conservative Conservative 2001-08-24 100.0%; 100.0%; 100.0%; R. Alec US/09/938,864 0 0 Score 51; Pred. No. Score 51; Pred. No. Mismatches Mismatches 51; DB 9; DB .7e+05; .7e+05; FOR 0 с ... WT1 WTI Length 9; Length 9; Indels Indels 0 0 Gaps Gaps 0 0 昂 QY QY

B US-10-125-635A-2 RESULT ; ORGANISM: Homo sapiens US-09-872-832-46 RESULT 5 US-09-872-832-46 ; TYPE: PRT ; ORGANISM: Mus musculus US-09-938-864-293 GENERAL INFORMATION: APPLICANT: Memorial Sloan-Kettering Cancer Center TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF FILE REFERENCE: 830002-2003.1 CURRENT APPLICATION NUMBER: US/09/872,832 CURRENT FILING DATE: 2001-06-01 PRIOR APPLICATION NUMBER: 60/209,157 PRIOR FILING DATE: 2000-02-06 NUMBER OF SEQ ID NOS: 49 SOFTWARE: PatentIn version 3.0 SEQ ID NO 46 NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for SEQ ID NO 2 GENERAL INFORMATION: Sequence 2, Application US/10125635A Publication No. US20030039635A1 Matches Query Match Best Local ( Sequence 46, Application U Patent No. US20020131960A1 Matches Query Match SOFTWARE: Fa SEQ ID NO 293 Best Local Similarity Matches 9; Conserv APPLICANT : APPLICANT : APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 APPLICANT: Cheever, Martin A. APPLICANT: WeNeill, Patricia D. APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 APPLICANT: Gaiger, Alexander APPLICANT: Smithgall, Molly D. CURRENT APPLICATION NUMBER: US/1 CURRENT FILING DATE: 2002-07-19 NUMBER OF SEQ ID NOS: 413 APPLIÇANT : APPLICANT : TYPE: PRT LENGTH: LENGTH: 1 RMFPNAPYL 9 **1 RMFPNAPYL 9** 1 RMFPNAPYL 9 1 RMFPNAPYL 9 l Similarity 9; Conserv ø FastSEQ for Windows Version 3.0 Carter, Darrick Application US/09872832 Spies, A. Gregory Boydston, Jeremy Evans, Lawrence Conservative Conservative for Windows Version 3.0 46] 100.0%; 100.0%; 100.0%; 100.0%; US/10/125,635A 0 <u>,</u> Score 51; Pred. No. Score 51; DB 9; Pred. No. 2.7e+05; Mismatches Mismatches 2.7e+05; DB 10; FOR WT1 <u>,</u> 0 Length 9; Length 9; Indels Indels <u>,</u> <u></u> Gaps Gaps 0 0

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RESULT 8 US-09-938-864-2 멼 Q US-10-125-635A-3 B QY ; ORGANISM: Homo sapien US-10-125-635A-2 ; ORGANISM: Mus musculus US-10-125-635A-3 RESULT Sequence 2, Application US/09938864 Publication No. US20030072767A1 APPLICANT: Gaiger, APPLICANT: McNeill APPLICANT: Smithga APPLICANT: Moulton GENERAL Best Local Similarity Matches 9; Conserv Query Match SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 Query Match Best Local : SEQ ID NO 2 Sequence Matches GENERAL Dublication No. US20010100635A NUMBER OF SEQ ID NOS: 413 SOFTWARE: FastSEQ for Windows Version 3.0 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 APPLICANT : APPLICANT : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 APPLICANT : NUMBER OF SEQ ID NOS: APPLICANT : APPLICANT: Gaiger, LENGTH: 23 TYPE: PRT **NPPLICANT**: **NPPLICANT**: LENGTH: 23 TYPE: PRT APPLICANT: APPLICANT: APPLICANT : APPLICANT : LENGTH: 23 TYPE: PRT PPLICANT : ORGANISM: Homo sapien 10 10 RMFPNAPYL 18 Local Similarity les 9; Conserv 1 RMFPNAPYL 9 **1** RMFPNAPYL 9 RMFPNAPYL 18 INFORMATION: INFORMATION: 23 23 Cheever, Martin A. McNeill, Patricia D. Sutherland, R. Alec Spies, A. Gregory Boydston, Jeremy Sleath, Paul R. Mossman, Sally Carter, Darrick Vedvick, Mouiton, Gus Smithgall, Molly Evans, Lawrence McNeill, Patricia D. Smithgall, Molly D. Conservative Conservative Alexander Alexander Thomas S. 46] 100.0%; 100.0%; 100.0%; 100.0%; 0 <u>;</u> Score 51; DB 9; Pred. No. 0.0087 Pred. Score 51; Mismatches Mismatches No. 0.0087 DB 9; 0 0 Length 23; Length 23; Indels Indels 0; 0 Gaps Gaps 0 0; B QY B QY US-09-938-864-2

; ORGANISM: Homo sapiens US-10-125-635A-343 RESULT 10 US-10-125-635A-343 ; LENGTH: 23 ; TYPE: PRT ; ORGANISM: Mus musculus US-09-938-864-3 US-09-938-864-3 RESULT 9 NUMBER OF SEQ ID NOS: 461 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 343 LENGTH: 152 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 23 Query Match GENERAL Sequence 343, Application US/10125635A Publication No. US20030039635A1 Matches 9; Conserv Query Match Query Match 100.0%; Best Local Similarity 100.0%; Matches 9; Conservative 0 GENERAL sequence CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT FILING DATE: 2002-07-19 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 APPLICANT : APPLICANT : APPLICANT: CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 413 APPLICANT : APPLICANT : APPLICANT: Gaiger, Alexander TITLE OF INVERTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 APPLICANT : APPLICANT : APPLICANT : APPLICANT: TYPE: PRT APPLICANT : APPLICANT: APPLICANT : APPLICANT : APPLICANT: APPLICANT: Gaiger, Alexander Jence 3, Application US/09938864 Lication No. US20030072767A1 10 RMFPNAPYL 18 10 RMFPNAPYL 18 1 RMFPNAPYL 9 1 RMFPNAPYL 9 INFORMATION: INFORMATION: Cheever, Martin A. McNeill, Patricia D. Sutherland, R. Alec Moulton, Gus Vedvick, Thomas S. Sleath, Paul R. Carter, Darrick Evans, Lawrence Spies, A. Gregory Boydston, Jeremy Smithgall, Molly D. Mossman, Sally McNeill, Patricia D. Smithgall, Molly Conservative 100.0%; 100.0%; 100.0%; Score 51; 0 ; 0 Score 51; DB 9; Pred. No. 0.0087; ); Mismatches 0; Score 51; DB 9; Pred. No. 0.0087; Mismatches DB 9; DB 9; Length 23; <u>,</u> WT1 Length 23; Length 152; Indels Indels <u>,</u> 0; Gaps Gaps

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Patent No. US20020082304A1 GENERAL INFORMATION: APPLICANT: Call, Katherine M. APPLICANT: Calser, Thomas M. APPLICANT: Buckler, Alan J. APPLICANT: Buckler, Jerry APPLICANT: Pelletier, Jerry APPLICANT: Haber, Daniel A. APPLICANT: Bruening, Wendy APPLICANT: Bruening, Wendy APPLICANT: Bruening, Wendy APPLICANT: Bruening, Wendy TITLE OF INVENTION: Localization TITLE OF INVENTION: Wilms, Tumoj FILE REFERENCE: 0050.1312-013 CURRENT APPLICATION NUMBER: US 09/1 PRIOR APPLICATION NUMBER: US 09/2 PRIOR APPLICATION NUMBER: US 09/2 PRIOR APPLICATION NUMBER: US 07/2 PRIOR FILING DATE: 1993-08-02 PRIOR APPLICATION NUMBER: US 07/2 PRIOR APPLICATION NUMBER: US 07/2 PR	Query Match         Best Local Similarity         Matches       9; Conser         Oy       1 RMFPNAPYL 9         Oy       1 RMFPNAPYL 9         Db       51 RMFPNAPYL 59         DS       51 RMFPNAPYL 59         RESULT 12         US-09-929-315-5         : Sequence 5. Applicatio	APPLICANT: Spies, A. Gregor APPLICANT: Spies, A. Gregor TITLE OF INVENTION: COMPOSIT TITLE OF INVENTION: SPECIFI FILE REFERENCE: 210121.465C5 CURRENT APPLICATION NUMBER: 0 CURRENT FILING DATE: 2001-0 NUMBER OF SEQ ID NOS: 413 SOFTWARE: FastSEQ for Window SEQ ID NO 343 LENGTH: 152 TYPE: PRT ORGANISM: Homo sapiens US-09-938-864-343	RESULT 11 US-09-938-864-343 ; Sequence 343, Applicati ; Publication No. US20030 ; Publication No. US20030 ; GENERAL INFORMATION: ; APPLICANT: Gaiger, Ale ; APPLICANT: McNeill, Pa ; APPLICANT: Smithgall, ; APPLICANT: Wedvick, Pa ; APPLICANT: Vedvick, Pa ; APPLICANT: Sleath, Pa ; APPLICANT: Steath, Pa ; APPLICANT: Steath, Pa	Matches 9; Conser Oy 1 RMFPNAPYL 9           Db 51 RMFPNAPYL 59
No. US20020082334A1 , INFORMATION: ANT: Call, Katherine M. ANT: Call, Katherine M. ANT: Glaser, Thomas M. ANT: Buckler, Jerry ANT: Buckler, Jerry ANT: Pelletier, Jerry ANT: Housenan, David E. ANT: Housenan, David E. ANT: Bruening, Wendy ANT: Bruening, Wendy ANT: Bruening, Wendy ANT: Darveau, Andre OF INVENTION: Localization and Characterization of the OF INVENTION: Wilms' Tumor Gene EFERENCE: 0050.1312-013 OF INVENTION: WMBER: US 09/037,179 FILING DATE: 1998-03-09 APPLICATION NUMBER: US 08/102,942 FILING DATE: 1998-08-02 APPLICATION NUMBER: US 07/614,161 FTLING DATE: 1990-11-13 APPLICATION NUMBER: US 07/435,780	ore 51; DB 9; Length 152; ed. No. 0.059; Indels 0; Mismatches 0; Indels 0;	: Spies, A. Gregory : Boydston, Jeremy INVENTION: COMPOSITIONS AND METHODS FOR WT1 INVENTION: SPECIFIC IMMUNOTHERAPY RENCE: 210121.465C5 INVALUE: 2001-08-24 ILLING DATE: 2001-08-24 SEQ ID NOS: 413 FastSEQ for Windows Version 3.0 152 152 152 154 152 152 154 155 155 155 155 155 155 155	43 Application US/09938864 D. US20030072767A1 AMTION: aiger, Alexander aiger, Alexander Smithgall, Patricia D. Smithgall, Molly Smithgall, Molly Moulton, Gus Vedvick, Thomas S. Sleath, Paul R. Vessman, Sally France Tauronce	Conservative 0; Mismatches 0; Indels 0; YL 9    YL 59
	Gaps			Gaps
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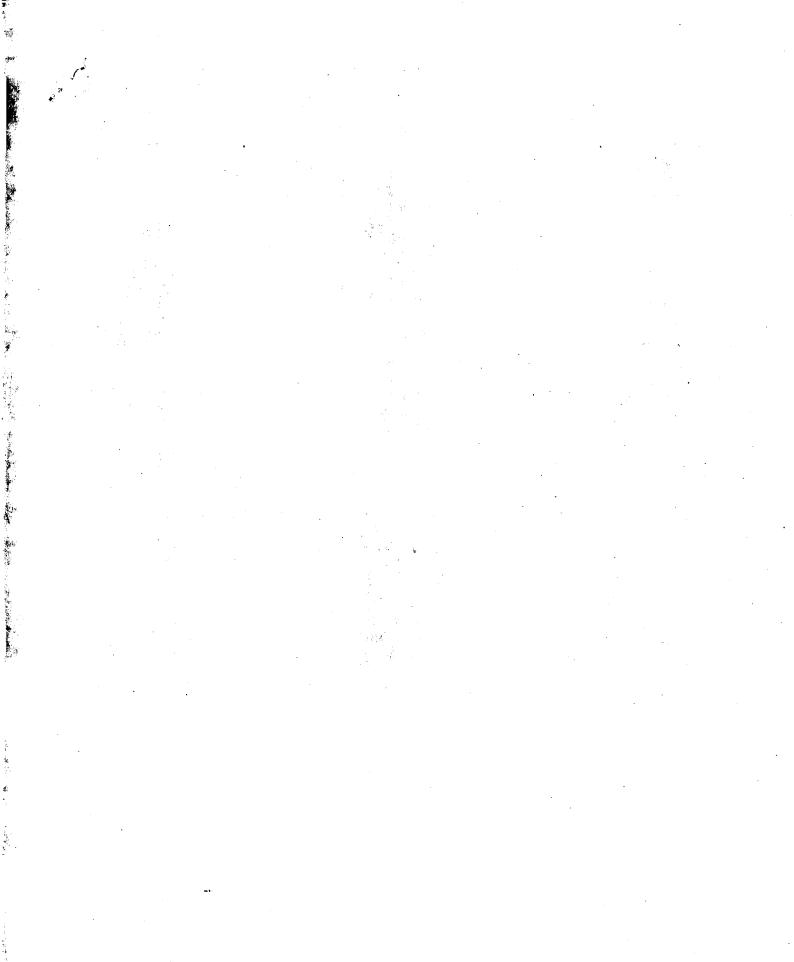
APPLICANY: Bruening, Werdy APPLICANY: Bruening, Werdy TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilns' Tunor Gene FILLE REFERENCE: 0050.1312-014 CURRENT AFPLICATION NUMBER: US/09/993,215 CURRENT FILING DATE: 2001-11-12 PRIOR APPLICATION NUMBER: US 09/037.179 PRIOR APPLICATION NUMBER: US 09/037.179 PRIOR FILING DATE: 1998-03-09 PRIOR FILING DATE: 1998-03-09 PRIOR FILING DATE: 1993-08-02 PRIOR FILING DATE: 1993-08-02 PRIOR FILING DATE: 1993-08-03 PRIOR FILING DATE: 1993-08-102,942 PRIOR FILING DATE: 1993-08-102,942 PRIOR FILING DATE: 1993-01-13 PRIOR APPLICATION NUMBER: US 07/614,161 PRIOR APPLICATION NUMBER: US 07/435,780 PRIOR FILING DATE: 1989-11-13 PRIOR FILING DATE: 1989-11-13 PRIOR FILING DATE: 1989-11-13 PRIOR FILING DATE: 1989-11-30 PRIOR FILING DATE: 1980-11-30 PRIOR FILING DATE: 1980-11-3 T 14 -125-635A-395 uence 395, Application US/10125635A lication No. US20030039635A1 JERAL INFORMATION: PLICANT: Gaiger, Alexander PLICANT: Smithgall, Molly D. PLICANT: Call, Katherine M. PLICANT: Call, Katherine M. PLICANT: Glaser, Thomas M. PLICANT: Ito, Caryn Y. PLICANT: Ito, Caryn J. PLICANT: Buckler, Alan J. / Match Local Similarity thes 9; Conserv: 1 RMFPNAPYL 9 |||||||| 40 RMFPNAPYL 48 1 RMFPNAPYL 9 |||||||| 40 RMFPNAPYL 48 ID NO 5 NGTH: 154 ID NO 5 NGTH: 154 NR APPLICATION NUMBER: US 07/795,323 NR FILLING DATE: 1991-11-20 LER OF SEQ ID NOS: 21 WARE: FastSEQ for Windows Version 4.0 E: PRT ANISM: Homo sapien 93-215-5 ICANT : es ANISM: Homo sapien 29-315-5 ER OF SEQ ID NOS: WARE: FastSEQ for nce 5, Application US/09993215 L No. US20020128196A1 93-215-5 13 Local Similarity ≥s 9; Conservat Match E: PRT ICANT : ICANT : ICANT : Pelletier, Jerry Haber, Daniel A. Rose, Elise A. Housman, David E. Conservative Conservative for Windows Version 4.0 21 100.0%; 100.0%; 100.0%; Score 51; DB 10 100.0%; Pred. No. 0.059; <u>,</u> 0 Score 51; DB 10; Length 154; Pred. No. 0.059; Mismatches Mismatches DB 10; 0 <u>.</u> Length 154; Indels Indels 0 <u>0</u> Gaps Gaps 0; 0 ;;

APPLICANT: Sutherland, R. Alec TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C7 CURRENT APPLICATION NUMBER: US/10/125,635A CURRENT APPLICATION NUMBER: US/10/125,635A SEO ID SEO ID NOS: 461. SOFTWARE: FastSEO for Windows Version 3.0 SEO ID NO 3955ED for Windows Version 3.0 LENGTH: 214 TYPE: PRT US-10-125-635A-395 CURRENT APPLICATION NUMBER: US/09/938,864 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 413 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 395 LENGTH: 214 TVPE: PRT ORGANISM: Homo sapiens US-09-938-864-395 B Q 망 QY Search completed: April 25, 2003, 06:57:02 Job time : 270 secs RESULT 15 US-09-938-864-395 Query Match 100.0%; Score 51; DB 9; Best Local Similarity 100.0%; Pred. No. 0.083; Matches 9; Conservative 0; Mismatches Query Match 100.0%; Best Local Similarity 100.0%; Matches 9; Conservative 0 Sequence 395, Application US/09938864 Publication No. US20030072767A1 GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: Evans, Lawrence APPLICANT: Spies, A. Gregory APPLICANT: Boydston, Jeremy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY FILE REFERENCE: 210121.465C5 APPLICANT : **NPPLICANT**: 1 RMFPNAPYL 9 |||||||| 59 RMFPNAPYL 67 1 RMFPNAPYL 9 |||||||| 59 RMFPNAPYL 67 59 à Gaiger, Alexander Carter, Darrick Cheever, Martin A. McNeill, Patricia D. Moulton, Gus Vedvick, Thomas S. Sleath, Paul R. Smithgall, Molly Mossman, Sally McNeill, Patricia D. <u>0</u> Score 51; DB 9; Length 214; Pred. No. 0.083; ; Mismatches 0; Indels DB 9; 0; Indels Length 214; 0 ;; 0 Gaps Gaps 0 ; 0

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es, their fragments or erapy -	998; 98GB-0023897. IMPERIAL COLLEGE INNOVATIONS LTD. J, Gao L; 0-376123/32. 0-376123/32. ptides comprising WT-1 and GATA-1 epitopes, t , useful as vaccines for cancer immunotherapy Page 74; 93pp; English.	OV-1 O-) SS H 200 200 200 1 pe ants	PR 02-NOV- XX PR 02-NOV- XX (IMCO-) XX Stauss XX PI Stauss DR WPI; 20 XX WPI; 20 XX Novel p PT variant XX Claim 1	Description Human cytotoxic T WT1 derived immuno Human Wiln's tumou Human Wiln's tumou Mouse Wiln's tumou Human WT1 immunoge Human WT1 immunoge Human WT1 immunoge	Length DB ID 9 21 AAY94202 9 21 AAY98670 9 21 AAY98670 9 21 AAY98778 9 21 AAY80200 9 22 AAU6877 9 22 AAU68877 9 22 AA062002 9 22 AA662102 9 23 ABG33239 9 23 ABG33347	Match 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	2 Score Score 5 Score 5 Score 5 Score 5 Score 5 Score 5 Score 5 Score 5 Score 5 Score 5	
	99₩О-GB03572.	piens. 6249-Al. 2000. 1999;	OS Homo sa XX PN WO20002 XX PD 11-MAY- XX PF 02-NOV- XX	ed by chance to have a f the result being printed, ore distribution.	number of results predicted by n or equal to the score of the r analysis of the total score d SUMMARIES	is the rived l guery	Pred. 1 score g and is	Result
peptide WT126-34. re; leukaemia; nunotherapy.	ALIGNMENTS peptide; 9 AA. t entry) tymphocyte-recognised WT1 lymphocyte-recognised WT1 anoma; ovarian cancer; imm	202 standard; 202; L-2000 (firs cytotoxic T cytotoxic T t cancer; mel	RESULT 1 AAY94202 ID AAY9420 AC AAY9420 XX AAY9420 XX AAY9420 DT 28-JUL- DT 28-JUL- DE Human c XX W Dreast XX breast	eqp emb1/AA1985.DAT:* eqp emb1/AA1986.DAT:* eqp emb1/AA1986.DAT:* seqp emb1/AA1988.DAT:* seqp emb1/AA1990.DAT:* seqp emb1/AA1991.DAT:* seqp emb1/AA1991.DAT:* seqp emb1/AA1993.DAT:* seqp emb1/AA1993.DAT:* seqp emb1/AA1993.DAT:* seqp emb1/AA1995.DAT:* seqp emb1/AA1996.DAT:* seqp emb1/AA1999.DAT:* seqp emb1/AA1999.DAT:* seqp emb1/AA1999.DAT:* seqp emb1/AA1999.DAT:*	<pre>/SIDS2/gcgdata/genesed/genesedp embl/AA1985.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1987.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1988.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1987.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1987.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1987.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1997.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1997.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1997.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1997.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1997.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1997.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1995.DAT:* /SIDS2/gcgdata/genesed/genesedp embl/AA1995.DAT:*</pre>			
Wilms' tumour wri var Lanc Wilms' tumour wri Human Wri protein, Wilms' tumour poly Human Wri protein Mouse Wri protein Human Wilm's tumou Human Wilm's tumou Human Wilm's tumou Human Wilm's tumou	429 16 AAR85065 429 23 ABG33400 449 21 AAW47176 449 21 AAY98805 449 21 AAY98805 449 21 AAY80196 449 21 AAY80196 449 21 AAY80197 449 22 AAU68900 449 22 AAU68904 449 22 AAU68197	51 100.0 51 100.0 51 100.0 51 100.0 51 100.0 51 100.0 51 100.0 51 100.0 51 100.0	444433333 5432₽098760	eqp-embl/AA1980.DAT:* eqp-embl/AA1981.DAT:* eqp-embl/AA1982.DAT:* eqp-embl/AA1983.DAT:* eqp-embl/AA1983.DAT:*	inimum Match 0% aximum Match 100% isting first 45 summaries /SIDS2/gcgdata/geneseq/genese /SIDS2/gcgdata/geneseq/genese /SIDS2/gcgdata/geneseq/genese /SIDS2/gcgdata/geneseq/genese		Post-processing: Database :	Post-pro Database
WT33 Wilm's tumour Human WT1-C. Homo Human WT1-C. Homo Human Trx_WT1_A. Human Ra12/WT1-F.	2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3		332 34 35 4	s: 908470	satisfying chosen parameters 1: 0 1: 2000000000	f hits length length	umber DB se DB se	Total n Minimum Maximum
Amino active pory Amino active sequence Wilms' tumour anti Human WT1-E. Homo Human WT1-A. Homo Human Ra12/WT1-E. Wilm's tumour poly	19223 1923 1923 1923 1923 1923 1923 1923		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		US-09-625-963-1 51 BLOSUM62 Gapop 10.0 , Gapext 0.5 908470 seqs, 133250620 residues		Title: Perfect score: Sequence: Scoring table: Searched:	Title: Perfect Sequency Scoring Searche
Human Jeukocyte an Human WT1 peptide Human WT1 peptide Human W11m's tumou Human W11 immunoge Human WT1 immunoge Human WT1 immunoge Human WT1 immunoge			220 220 210 210 210 210 210 210 210 210	5.1.4_p5_4578 Compugen Ltd. arch time 75 Seconds without alignments) 5.990 Million cell updates/sec	GenCore version 5.1.4_p Copyright (c) 1993 - 2003 Compuge in search, using sw model ril 25, 2003, 06:36:22 ; Search ti (without 15.990 Mi	Copy; protein se April :	ein -	OM prot Run on:
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888888888888888888888888888888888888888	PA PA PA PT PT	PR XX PX PX XX	Db RESULT AAY986 AC AC AC AC AC AC AC AC AC AC AC AC AC	*** 8*** 8****************************
Claim 4; Page 171; 193pp; English. The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WT1, (or variants of the immunogenic portion retaining the ability to react with WT1-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WT1 polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, mimetics or polynucleotides can be included with a carrier/excipient in pharmaceutical compositions or with a not specific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to enhance or induce an immune response specific for WT1 or a cell	<pre>(CORI-) CORIXA CORP. (GAIG/) GAIGER A. Gaiger A, Cheever M; WPI; 2000-293107/25. Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer -</pre>	, immunotherapy; immunogenic; malig static disease; mouse; human; Wilm cine. o sapiens. 00018795-A2. APR-2000. SEP-1999; 99WO-US22819. SEP-1999; 99WO-US22819. SEP-1999; 99US-0164223. MAR-1999; 99US-0276484.	1 AY AY	The present sequence is peptide epitope WT126-34, produced by WT1 expressing cells and found at residues 126-134 of the WT1 protein, which is recognised by cytotoxic T lymphocytes. WT1 is aberrantly expressed in leukaemias, breast cancer, melanoma and ovarian cancer. The peptide can be used as a vaccine to stimulate the elimination, by cytotoxic T lymphocytes, of cancer cells aberrantly expressing WT1. In addition, the nucleic acid encoding the peptide may also be used in the same manner. Alternatively, the peptide may be used in vitro to produce activated cytotoxic T lymphocytes. Sequence 9 AA; Ouery Match 100.0%; Score 51; DB 21; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC The present invention describes polypeptides (I) comprising an CC immunogenic portion of a native Wilm's Tumour gene product polypeptide, CC wr1, (or variants of the immunogenic portion retaining the ability to CC react with Wr1-specific antisera and/or T-cell lines or clones) and CC polypeptide. The polypeptides are useful therapeutically and to CC patients. The polypeptides are useful therapeutically and to polypeptide. The polypeptides are useful therapeutically and to cc patients. The polypeptides mimetics or polynucleotides can be included CC non-specific immune response enhancer (e.g. an adjuvant or enhancer CC enhance or induce an immune response specific for Wr1 or a cell CC enhance or induce an immune response specific for Wr1 or a cell CC enhance or induce an immune response specific for Wr1 or a cell CC expressing Wr1, useful to inhibit the development of malignant diseases associated with Wr1 expression, e.g. leukemia (especially acute/chronic CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially		vaccine. Mus musculus. W0200018795-A2. 06-APR-2000. 30-SEP-1999; 99WO-US22819. 30-SEP-1999; 98WS-0164223. 25-MAR-1999; 99US-0276484. (CORI-) CORIXA CORP. (GAIG/) GAIGER A.	B6A	expre assoc myelo breas AAY98 AAAY98 Prese Seque Seque Best Loc Matches

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XX XX KW Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen;	
IO-JAN-2002 (IIISC CHILY)	
16-TAN-2002 ( first	1 EMERNADYI Q
ID AAU68877 standard; Peptide; 9 AA. XX AC AAU68877;	Ouery Match     100.0%; Score 51; DB 21; Length 9;       Best Local Similarity     100.0%; Pred. No. 7.8e+05;       Matches     9; Conservative     0; Mismatches       0:     1ndels     0; Gaps
RESULT 6 AAU68877	Sequence 9 AA;
Db 1 RMFPNAPYL 9	cancer. The present sequence represents a peptide from the l Wilms' tumour suppressor gene WT1 product.
QY 1 RMEPNAPYL 9 .	
Query Match 100.0%; Score 51; DB 22; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC peptides, for cancer vaccines in treating leukaemia and solid tumours. CC The cancer antigens are useful for cancer vaccines in treating CC Leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma, CC multiple myoloma, stomach cancer, cancer of the large intestine. Jung
Sequence 9 AA;	
	PS Claim 5; Page 18; 48pp; Japanese. xx
CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL), CC myelodysplastic syndromes, myeloproliferative syndromes and cancers CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals, CC preferably humans. The present sequence is an articenic peoplide of	PT Cancer antigens based on Wilm's tumor suppressor gene WT1 product or PT peptide derivatives, for cancer vaccines in treating leukemia and solid PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer XX
	DR WPI; 2000-195264/17.
	PI Sugiyama H, Oka Y; xx
CC first isotated peptide, of between 9 and 40 analysis drugs of a first CC nucleic acid, encoding the peptide, in the manufacture of a medicament CC for treating or preventing mesotheliona. The peptides are antigenic	PA (SUGI/) SUGIYAMA H. XX
	ΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥ
PS Claim 1; Page 176; 242pp; English. vv	PF 30-JUL-1999; 99WO-JP04130.
PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic PT fragments - yy	
XX PT Composition for the treatment of mesothelioma comprises specific	W020(
DR WPI; 2001-648218/74.	OS Homo sapiens.
PI Cheever MA, Gaiger A; vv	major histocompatibility complex; leukaemia; tumour; antitumo
PA (CORI-) CORIXA CORP.	r suppressor dene. WT1. cancer, antiden, vaccine. W
PR 22-FEB-2000; 2000US-184070P. XX .	Human Wilms' tumour
РF 22-FEB-2001; 2001WO-US05702. XX	
PD 30-AUG-2001. XX	
PN WO200162920-A2. XX	AAY80200 . ID AAY80200 standard; Peptide; 9 AA.
OS Homo sapiens. XX	RESULT 4
<pre>KW leukaemia; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML; KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes; KW myeloproliferative syndrome; cancer; cytostatic. xx</pre>	QY     1 RMEPNAPYL 9       Db     1 RMEPNAPYL 9
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TO OWN 2002 (TITSE GUELY)	100.0%; Score 51; DB
AAU68/69;	Sequence 9 AA;
RESULT 5 AAU68769 ID AAU68769 standard; Peptide; 9 AA. XX AAU68769	CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). CC AAY98501 to AAY98811 represent polypeptide sequences, and AAA13848 to CC AAA13862 represent PCR primers, used in the exemplification of the CC present invention.
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Source coccecce coccecce and a set of the se Ð AAG62002 망 Ŷ RESULT 7 Matches Query Match Best Local The invention relates to the use of a composition comprising at least a first isolated peptide, of between 9 and 40 amino acids or a first nucleic acid, encoding the peptide, in the manufacture of a medicament for treating or preventing mesothelioma. The peptides are antigenic peptides derived from the Wilms' tumour protein WT1. The composition is useful for the treatment of mesothelioma, Wilms' tumour, preferably pleural mesothelioma and other WT1 associated malignancies e.g. leukaemia (including acute myeloid leukaemia, ALL, and childhood ALL), mesotheliona, CLL, acute lymphocytic leukaemia, ALL, and childhood ALL). Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's chromosome 11p13; zinc finger transcription factor. Human WT1 06-JUL-2001 myelodysplastic syndromes, myeloproliferative syndromes and cancers (e.g. breast, testicular, prostate, lung and ovarian) in mammals, preferably humans. The present sequence is an antigenic peptide of the invention derived from mouse WT1. Composition for the treatment of mesothelioma comprises specific peptides i.e. Wilms' tumour antigen polypeptide derived antigenic 04-OCT-1999; 04-OCT-2000; 2000WO-US27465 12-APR-2001 AAG62002; AAG62002 standard; Sequence Claim 1; Page WPI; 2001-648218/74. Cheever W0200125273-A2 ното fragments (CORI-) CORIXA CORP 22-FEB-2000; 2000US-184070P 22-FEB-2001; 2001WO-US05702. 30-AUG-2001 WO200162920-A2 Mus musculus. myeloproliferative acute lymphocytic leukaemia; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML ч 1 RMFPNAPYL 9 sapiens RMFPNAPYL 9 Similarity 9; Conser MA, immunogenic peptide SEQ ID 9 Conservative AA; (first Gaiger 24; 242pp; English 99US-0157459 leukaemia; Peptide; syndrome; A; entry)  $100 \\ 100$ .0%; .08; ø 0; Score 51; Pred. No. cancer; cytostatic. ALL; myelodysplastic syndromes; AA Mismatches 51; NO: 185 7.8e+05; DB 22; 0 Length 9; Indels tumour 0 Gaps gene; įs <u>م</u> 0; RESULT 8 AAG62110 Ъ QY Query Match Best Local : Matches The present invention describes compositions comprising peptides derived from the Wiln's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a polypeptide described in the exemplification of the invention. Polypeptide comprising part of the Wilm's Tumour gene product sequence used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI  $\,$ Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene; chromosome 11p13; zinc finger transcription factor. Polypeptide comprising part of the Wilm's Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI  $\,$  -WPI; Claim 4; Page 200; 228pp; English. WPI; 2001-328324/34 Skeiky YAW, 04-OCT-1999; 04-OCT-2000; 2000WO-US27465 12-APR-2001 WO200125273-A2 Mus musculus Mouse WT1 immunogenic peptide 06-JUL-2001 AAG62110; AAG62110 standard; Sequence Claim 4; Page 183; 228pp; English. Skeiky YAW, (CORI-) CORIXA (CORI-) CORIXA CORP 1 RMFPNAPYL 9 |||||||| 1 RMFPNAPYL 9 2001-328324/34 Similarity 9; Conserv 9 Conservative хu AA; Хu (first entry) CORP 99US-0157459 ć Ļ Peptide; Cheever MA, Cheever MA, 100 .08; .08; 9 <u>,</u> Score Pred. A SEQ ID NO: Mismatches Reed Reed NO ; SG SG; DB 22; 7.8e+05; 293. 0 Indels <sup>‡</sup> Length ف 0 Gaps İs 0

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RESU	Qy Db	MBRQ	SQ	888888	PT PS XX	DR XX	PA	PR PR XX PA	PR	PD XX	X PN	x o x x	KWXX	DE X DI X AC	XXD	RESU	υb	, ç	A Mark	n O	SQ	888	1
RESULT 10 ABG33347	1 RMFPNAPYL 9           1 RMFPNAPYL 9	Query Match 100.0%; Score 51; DB 23; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 9 AA;	The invention relates to an isolated WT1 polynucleotide (I) and polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are used for treating and detecting cancer in a patient, and for stimulating an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid sequences of the invention.	Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient - Example 4; Page 194; 260pp; English.	Sleath PR, Mossman S, Evans L, Sples AG, Boydston J; WPI; 2002-352217/38.	A MONGETT DD GmithGell M Monltop G Volation HG.	2000; 2000US-0685830. 2001; 2001US-0785019. 2001; 2001US-0938864. CORIXA CORP.	2000US-0684361.	11-APR-2002. 03-CCT-2001; 2001WO-US31139.	WO200228414-A1.	Ω0	; mouse; cytostatic; immu e response.	ABG33239; 15-JUL-2002 (first entry) Human WT1 immunogenic peptide #162.	3239 standard; Peptide; 9 AA.	RESULT 9	INTERNALL 2	1 KMEVNADYI 0 	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	0%; Score 51; DB 22; Length 9; 0%: Brod NO 7 Re+05.	Sequence 9 AA;	immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a polypeptide described in the exemplification of the invention.	
PN ( XX				RESULT 11 AAE17298 ID AAE1 XX AC AAE1	Qу Db	Que Best Mato		88888			DR V								KW			ACXID	
Homo sapiens. WO200194944-A2.	rumman renverse ancusen; mayor miscocompaciantis complex, mac, cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour; immune response; cancer.		18-APR-2002 (first entry)	JT 11 1298 AAE17298 standard; peptide; 9 AA. AAE17298;	1 RMEPNAPYL 9           1 RMEPNAPYL 9	Ouery Match 100.0%; Score 51; DB 23; Length 9; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 9 AA;	The invention relates to an isolated WT1 polynucleotide (I) and polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are used for treating and detecting cancer in a patient, and for stimulating an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid sequences of the invention.	Example 4; Page 210; 260pp; English.	Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient -	WPI; 2002-352217/38.	Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS; Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;	(CORI-) CORIXA CORP. (GAIG/) GAIGER A.	06-OCT-2000; 2000US-0684361. 09-OCT-2000; 2000US-0685830. 15-FEB-2001; 2001US-0785019. 24-AUG-2001; 2001US-0938864.	03-OCT-2001; 2001WO-US31139.	11-APR-2002.	WO200228414-A1.	Mus musculus.	Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.	Mouse WT1 immunogenic peptide #44.	15-JUL-2002 (first entry) .	ABG33347 standard; Peptide; 9 AA. ABG33347;	1

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<ul> <li>13-DEC-2001.</li> <li>13-DEC-2001. 2001NO-USI791.</li> <li>24. Conversion 2001NO-USI791.</li> <li>25. Sachalan M. Latouche J.</li> <li>25. Sachalan M. Latouche J.</li> <li>26. Writ 2002-139667/18.</li> <li>27. Sachalan M. Latouche J.</li> <li>28. Writ 2002-139667/18.</li> <li>29. Artificial antigen presenting cells for activating in presenting complex having beda7-microglobulin. exogenous accessory molecule, human leukocyte presenting complexing beda7-microglobulin. accessory molecule.</li> <li>20. The present investion relates to an artificial antigen presenting cells for activating complexing beda7-microglobulin. an exogenous accessory molecule.</li> <li>20. The present investion relates to an artificial antigen presenting complexing beda7-microglobulin. an exogenous accessory molecule.</li> <li>20. The present investion relates to an artificial antigen presenting complexing beda7-microglobulin. an exogenous accessory molecule.</li> <li>20. The present investion relates to an artificial antigen presenting complexing the start set is proceed and investing the start set is proceed and investion of relativation of relativati</li></ul>			YD XX
<pre>11-DEC 2001. 11-DEC 2001. 01-JUN 2001; 200105-20915PF. (SLOK ) SLOAM KETTERING INST CANCER RES. Sadelain M. Latouche J; WPI: 202-13967/18. Artificial antigen presenting cells for activating T lymphorytes, comprises eukargetic cell expressing antigen presenting cell (APC) comprising eukargetic cell expressing antigen presenting cell (APC) comprising eukargetic cell expressing an attigen presenting complex comprising beta2-microglobuli, an exogenous accessory molecule, human leakocyte antigen molecule and profein (APC) comprising beta2-microglobuli, an exogenous accessory molecule complex comprising to a studien presenting cell (APC) comprising beta2-microglobuli, an exogenous accessory molecule a human leakocyte attigen, HL (major histocompatibuty complex, MHC) a buent (for identify) within a test population of cytotoxic receives, contactive to a specific elly processe. The invention also relates to methods for activation of the superset. APC is a specific antigen (TCL) within is useful for idenmostic purposes. APC is a provide the tradient criate activation of expresses. APC is there primery cell activation include cell-based assays for quantifying imune response in normal. Infected or treated (vaccinated) patients. Composition of primery for antitumeur response. The investidation of primery for the treatment of cancer. The present devectinated patients is used for the treatment of cancer. The present of crist sequence 9 AN: sequence 9 AN: sequence 9 AN: settodes 5; Conservative 0; Mismatches 0; Tudels 0; Caps in NFPNAPHL 9 i NFP</pre>		HOIID W0200	PN
<pre>13-DEC-2001. 01-JUK-2001; 2001Wo-US17981. 02-JUK-2000; 2000WS-209157P. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain M. Latouche J: WPT: 2002-139667/18. Artificial antigen presenting cells for activating T lymphocytes. comprises evaluation: coll expressing antigen presenting complex having beta2-microglobulin, exogenous accessory molecule, human leukocyte antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen presenting cell (AAPC) comprising a eukaryotic cell expressing an antigen presenting cell complex comprising a eukaryotic relates to an artificial antigen presenting cell (AAPC) comprising a eukaryotic relates to an artificial antigen presenting cell scale of a single type and appresenting cells. The metrod is also uncluse of a single type and sporter intervention also uncluse of a single type and appresenting cell (cancellular) to produce an ecogenous i cell-specific epitope. The invention is also uncluse of a composition protein the sporter intervention also uncluse and diagnotic applications intrable processed intracellular) to produce an ecogenous i coll sporter intervention also uncluse is used for the treatment of cancer: The present sequence is activation. Sequence 9 AA: Sequence 9 AA: Seq</pre>	dısease; cancer; ımour; immune resp	WTL; lumunocherapy; lumunogen1c; malignant metastatic disease; mouse; human; Wilm's tu vaccine.	A K K K K
<pre>13-DEC-2001. 01-JUN-2001; 2001WO-USI7981. 02-JUN-2000; 2000US-209157P. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J; WPI: 2002-139667/18. ArtLificial antigen presenting cells for activating T lymphorytes, Comprises enkaryotic cell acycessing antigen presenting complex having beta2-microglobulin, exceptions accessory molecule, human leukocyte antigen molecule and protein - Example 17; Page 40; 75p; English. The present invention relates to an artIficial antigen presenting cell (AAPC) comprising a eukaryotic cell expressing an antigen presenting cell complex on molecule and protein - man leukocyte and a protein that is proceeded intracellular complex on exogenous T cellseper the presenting cell (AAPC) comprising beta2-microglobule, an exogenous accessory molecule complex is a single type and a protein that is proceeded intracellular to produce an exogenous T cellseper the protocytes. The invention also relates to methods for activation of T imphosytes. The method is also threatign of primary T cell activation and dispositic applications in a source of a superior contracting APPC with a suitable population of T imphorytes uper local activations and tagnostic applications investigation of T humphorytes of antigen and accessory molecules, and diagnostic applications suitable for the activation and isonetic applications include cell-based assays for guantifying immue response in normal, infected or treated (vaccinated) patients. Composition applications of the present sequence is human HLA-A2.1 restricted peptide used in additional AAPC induced CTL- activation. Sequence 9 AA; Netry Match automs 0; Kismatches 0; Mismatches 0; Tadels 0; Gaps 1 MMFNAPYL 9 1 MMFNAPYL 9 1 MMFNAPYL 9 2 NMFNAPYL 9 2 NMFNAPY</pre>	:	Human WT1 peptide SEQ ID NO:2.	DE
<pre>13-DEC-2001. 01-UW-2001; 2001WO-USI7981. 02-UW-2000; 2000WS-209157F. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J; WPI: 2002-139667/18. Artificial antigen presenting cells for activating T lymphorytes, comprises enkaryotic cell expressing antigen presenting cemplex having beet2-microglobulin, ecogenous accessory molecule, human leukocyte antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen presenting cell (AAPC) complising a eukaryotic cell expressing an antigen presenting complex comprising a eukaryotic sell expressing an antigen presenting cell (AAPC) complising a eukaryotic sell expressing an antigen presenting complex to methods for activation of T lymphorytes. The invention also relates to methods for activation of T lymphorytes. The invention also relates and diagnostic applications include call-based aspostic applications investigation of primary T cell activation and dispostic applications investigation of T sumphorytes in normal, infected or treated (vaccinated) patients. Composite opplication and throw or relises and coessions invention is used for the treatment of cancer. The present sequence is activation activation. Sequence 9 AA; Duery Match estruction i NMFPNAPYL 9 1 NMFPNAPYL</pre>		31-JUL-2000 (first	XG
<pre>13-DEC-2001. 01-JUN-2001; 2001W0-US17981. 02-JUN-2000; 2000US-209157P. (SLOK) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J; WPI; 2002-139667/18. Artificial antigen presenting cells for activating T lymphotytes, comprises eukaryotic cell expressing antigen presenting complex having beta7-microglobilin, exogenous accessory molecule, human leukoryte antigen molecule and protein (APC) comprising beta7-microglobulin, an exogenous accessory molecule, human leukoryte numen leukoryte antigen trigen presenting cell specific all antigen presenting cell (APC) comprising beta7-microglobulin, an exogenous accessory molecule, numen leukoryte antigen trigen antigen presenting cell (APC) comprising beta7-microglobulin, an exogenous accessory molecule, a human leukoryte antigen trigen brise protein that is processed intracellular to produce an exogenous T cell aspecific aplicate accessory for invention also relates to methods for activation of T imphorytes. The invention also relates to methods for activation of T imphorytes that a substitute of a single type and a protein that is processed intracellular to produce an exogenous T cell activation and diagnostic purposes. APC is useful for identifying within a test population of cytotoxic T is antigen gravity cell activation and diagnostic purposes. APC is notecules, and diagnostic or applications include coll-based asays for quantifying immune response in normal, infected or cell-based asays for collecules and accessory of antitumour response. The briatenite disculated putients is used for the treatment of cancer. The present sequence is human itA-A2.1 restricted peptide used in additional AAPC-induced CTL- activation. Sequence 9 AN: Description of prime of the cell based asays for concervative 0; Mismatches 0; Indels 0; Gaps 1 MHEPNAPYL 9 1 MHEPNAPYL 9 1 MHEPNAPYL 9 1 MHEPNAPYL 9 1 MHEPNAPYL 9 1 MHEPNAPYL 9 1 MARCHARCE 1 Concervative 0; Mismatches 0; Indels 0; Gaps 1 MAY98502 standard; Peptide; 23 AA.</pre>			X A S
<pre>13-DEC-2001. 01-JUN-2001; 2001W0-US17981. 02-JUN-2000; 2000US-209157P. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J: WPI: 2002-139667/18. Artificial antigen presenting cells for activating T lymphocytes, comprises eukaryotic cell expressing antigen presenting complex having beta2-microglobulin, exogenous accessory molecule, human leukocyte antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen presenting cell (AAPC) comprising beta2-microglobulin, an exogenous accessory molecule, numan leukocyte a human leukocyte antigen, HLA (major histocompatibility complex lawing beta2-microglobulin, an exogenous accessory molecule, human leukocyte a human leukocyte antigen, Presenting cell (APC) comprising beta2-microglobulin, an exogenous accessory molecule, a human leukoryte antigen, HLA (major histocompatibility complex, HLC is perific antigen (TLS), which is useful for disgnostic, purpases. AMPC is also useful for identifying within a test population of cytotoxic T lymphocytes (TLS), which is useful for diagnostic application and isolating the activation allow discovery of antigens and accessory molecules, and dispostic applications include cell-based asaays for quantifying immune response in normal, infected or cells produced by intinsing AAPC is useful for allow discovery of antigens entice applications here primary T cell activation and antitumor response. The invention is used for the treatment of cancer. The present sequence is human HLA-2.1 restricted peptide used in additional AAPC-induced CTL- activation. Sequence 9 AA; usery Match success 9; Conservative 0; Mismatches 0; Indels 0; Gaps 11 RMFPNAPYL 9</pre>		SULT 12 Y98502 AAY98502 standard; Peptide; 23	AA
<pre>13-DEC-2001. 01-JUN-2001: 2001WO-USI7981. 02-JUN-2000: 2000US-209157P. (SLOR ) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J; WPI: 2002-139667/18. Artificial antigen presenting cells for activating T lymphocytes, comprises eukaryotic cell expressing antigen presenting complex having beta2-microglobulin, exogenous accessory molecule, human leukocyte antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen presenting cell (APC) comprising a eukaryotic cell expressing an antigen presenting complex comprising type and a protein that is processed intracellular (apc) complex (CTLS), which is useful for diagnostic processed intracellular problex (Strift) for activation of T lymphocytes. The method is also relates to methods for activation of T lymphocytes. The method is also useful for identifying within a test population of sylotoxic T lymphocytes (CTLS), which is useful for diagnostic processed intracellular population of p lympary T cell activation and diagnostic applications investigation of primary T cell activation and diagnostic applications here primary T cell activation allow discovery of antigens and accessory molecules, and diagnostic for allow discover; of antigens and accessory patients. Compositing the subsetul for cells proteined by invention is used for the treatment of cancer. The present sequence is human HLA-A2.1 restricted peptide used in additional AAPC-induced CTL- activation. Sequence 9 AA; Duery Match Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps (applicative 0; Matches 0; Indels 0; Indels 0; Caps (applicative 0; Matches 0; Indels 0; Indels 0; Caps (applicative 0; Matches 0; Indels 0; Caps (applicative 0; Matches 0; Indels 0; Caps (applicative 0; Matches 0; Indels 0; Caps</pre>		1 RMFPNAPYL          1 RMFPNAPYL	Qу
<pre>13-DEC-2001. 01-JUN-2001; 2001WO-US17981. 02-JUN-2000; 2000US-209157P. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain W, Latouche J; WPI; 2002-139667/18. Artificial antigen presenting cells for activating T l comprises eukaryotic cell expressing antigen presentin beta2-microglobulin, exogenous accessory molecule, hum antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen (AAPC) comprising beta2-microglobulin, an exogenous a human leukocyte antigen, HLA (major histocompatibili molecule of a single type and a protein that is proces to produce an exogenous T cell-specific ally aptibility specific antigen (TCA), which is useful for diagnostic also useful for activating CTLs, by contacting AAPC within a test population of T lymphocytes under conditions suitable and isolating the activated CTLs. Apc is further useful population of primary T cell activation and diagnostic investigation of primary T cell activation and diagnostic composition suseful for activated cells. Apc is further useful nolecules, and diagnostic applications and diagnostic investigation is useful for eliciting an anti- nument response in normal, infected or tre patients. Composition comprising AAPC or activated T c- utilising AAPC is useful for eliciting an anti- nument HLA-A2.1 restricted peptide used in additional A activation.</pre>	51; DB 23; Length 9; No. 7.8e+05; natches 0; Indels 0; Gaps	100.0%; Score 51; DB 23 Similarity 100.0%; Pred. No. 7.8e+C 9; Conservative 0; Mismatches	7
<pre>13-DEC-2001. 01-JUN-2001; 2001WO-US17981. 02-JUN-2000; 2000US-209157P. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J; WPI; 2002-139667/18. Artificial antigen presenting cells for activating T l comprises eukaryotic cell expressing antigen present beta2-microglobulin, exogenous accessory molecule, hum antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen (AAPC) comprising a eukaryotic cell expressing an atti complex comprising beta2-microglobulin, an exogenous a a human leukocyte antigen, HLA (major histocompatibili molecule of a single type and a protein that is proces to produce an exogenous T cell-specific epitope. The i relates to methods for activation of T lymphocytes. The useful for identifying within a test population of cyti specific antigen (TCA), which is useful for diagnostic and isolating the activating CTLs, by contacting AAPC is useful for identifying the activation allow discovery of anti molecules, and diagnostic applications in for diagnostic and isolating the activated CTLS. AAPC is further usef investigation of primary T cell activation and diagnost per primary T cell activation allow discovery of anti molecules, and diagnostic applications an infected or tre patients. Composition comprising AAPC or activated T c utilising AAPC is useful for the treatment of cancer. The pre human HLA.A2.1 restricted peptide used in additional A activation.</pre>		Sequence 9	SQ
<pre>13-DEC-2001. 01-JUN-2001; 2001WO-US17981. 02-JUN-2000; 2000US-209157P. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J; WPI; 2002-139667/18. Artificial antigen presenting cells for activating T l comprises eukaryotic cell expressing antigen present in beta2-microglobulin, exogenous accessory molecule, hum antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen (AAPC) comprising beta2-microglobulin, an exogenous a human leukocyte antigen, HLA (major hiscocompatibili molecule of a single type and a protein that is proces to produce an exogenous T cell-specific epitope. The i relates to methods for activation of T lymphocytes. The useful for identifying within a test population of cyt lymphocytes (CTLS), CTLs specifically activated agains specific antigen (TCA), which is useful for diagnostic also useful for activating CTLs. AAPC is further usef investigation of primary T cell activation and diagnost population of primary T cell activation and diagnost investigation of primary T cell activation and diagnost per primary T cell activation allow discovery of anti molecules, and diagnostic applications infected or tre patients. Composition comprising AAPC or activated T c utilising AAPC is useful for eliciting an antiuncy T cell activation population is useful for eliciting and many discovery of anti molecules, and diagnostic applications and diagnost antiume response in normal, infected or tre patients. Composition comprising AAPC or activated T c utilising AAPC is useful for eliciting an antiuncy T cell activation and the function T the present of the prime to activate application sinclude cell-ba guantify the activated the trestment of cancer T who normal the prime the trestment of cancer T who normal the prime the trestment of another the prime the trestment of an antivated T the prime the prime the prime the prime the prime</pre>	sed in additional AAPC-induced CTL-	human HLA- activation	\$888
<pre>13-DEC-2001. 01-JUN-2001; 2001WO-US17981. 02-JUN-2000; 2000US-209157P. (SLOK ) SLOAN KETTERING INST CANCER RES. Sadelain M, Latouche J; WPI; 2002-139667/18. Artificial antigen presenting cells for activating T l comprises eukaryotic cell expressing antigen present beta2-microglobulin, exogenous accessory molecule, hum antigen molecule and protein - Example 17; Page 40; 75pp; English. The present invention relates to an artificial antigen (AAPC) comprising beta2-microglobulin, an exogenous a nolecule of a single type and a protein that is proces to produce an exogenous T cell-specific ally activated agains specific antigen (TCA), which is useful for diagnostic also useful for identifying within a test population of crispication of specific antigen (TCA), which is useful for diagnostic and isolating the activation allow discovery of anti molecules, and diagnostic applications suitable and isolating the activation allow discovery of anti population of T lymphocytes under conditions suitable and isolating the activation allow discovery of anti molecules, and diagnostic application is possible activation allow discovery of antipication of primary T cell activation allow discovery of anti antice and diagnostic applications in table activation investigation of primary T cell activation allow discovery of anti antice activated CTISS. APC to activate useful for the useful antifying immune response in normal. Infected or tree investigation of primary T cell activation allow discovery of anti- antice activated criss and diagnostic applications and di</pre>	PC or activated T cells produced by	patients. utilising	388
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WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia; metastatic disease; mouse; human; Wilm's tumour; immune response; vaccine.	Mouse WT1 peptide SEO ID NO:3.	31-JUL-2000 (first entry)	AAY98503;	JLT 13 18503 AAY98503 standard; Peptide; 23 AA.	10 RMFPNAPYL 18	1 RMFPNAPYL 9	Query Match 100.0%; Score 51; DB 21; Length 23; Best Local Similarity 100.0%; Pred. No. 0.006; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps	Sequence 23 AA;	invention.	2 represent PCR primers, used in the exemplification of the	AAV98811 represent polymentide	l leukemia or acute lymphocytic leu	pression, e.q.	n immune response specific for WT1 or a cell	3 can be administered to human patients to	non-specific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T cell response) in vaccines. Pharmaceutical	<pre>&gt;r/excipient in pharmaceutical compositions</pre>	The polymontides minutice or polymonia an immune response	. The polypeptides are useful therapeutically and to	with wir-specific antisera a lsing 16 consecutive amino a	anticers and for m-cell lines or clo	ogenic portion of a		Claim 4; Page 46; 193pp; English.	l for inhibiting the develo d with WT1 expression e.g.	eptides comprising an immunogenic portion c	WPI; 2000-293107/25.	Gaiger A, Cheever M;	(CORI-) CORIXA CORP. (GAIG/) GAIGER A.	30-SEP-1998; 98US-0164223. 25-MAR-1999; 99US-0276484.	30-SEP-1999; 99WO-US22819.

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RESULT 14 AAU68601 ID AAU68601; XX AAU68601; XX AAU68601; XX Human Wilm's tumour protein, WT1, antigenic peptide #2. XX Human; Wilms' tumour; WT1; pleural mesothelioma; antigen; XX Human; Wilms' tumour; WT1; pleural mesothelioma; antigen; XX Human; Wilms' tumour; WT1; pleural mesothelioma; antigen; XX Human wilm's acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML; Acute lymphocytic leukaemia; ALL; myelodysplastic syndromes; Homo sapiens. XX W w0200162920-A2. XX Y2 -FEB-2001; 2001WO-US05702. XX Y2 -FEB-2000; 2000US-184070P. XX (CORI-) CORIXA CORP.	e 23 AA; h 100.0%; Score 51; DB 21; Length 23; Similarity 100.0%; Pred. No. 0.006; 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; FPNAPYL 9         FPNAPYL 18	<pre>29-MAP-1999; 99US-0276484. (CORI-) CORIXA CORP. (GAIG/) GAIGER A. Gaiger A, Cheever M; WPI; 2000-293107/25. Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer - Example 3; Page 46; 193pp; English. The present invention describes polypeptides (I) comprising an immunogenic portion of a native W11m s Tumour gene product polypeptide, useful for variants of the immunogenic portion retaining the ability to react with WT1-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (a) or less of a native WT1 polypeptide. The polypeptides are useful therpetically and to nanufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, mimetics or polynuclectices can be included with a carriter/exclpient in pharmaceutical compositions or with a compositions and vaccines can be administered to human patients to expressing WT1, useful to inhibit the development of malignant diseases associated with WT1 expression, e.g. leukemia (especially acute/chronic myeloid leukemia very or a cuete inphocytic leukemia) or cancer (especially secuted with WT1 expression, e.g. leukemia (especially especially enhanced polypeptides and administered to man patients to enhance or induce an immune response specific for WT1 or a cell with a carriter/exclude the development of malignant diseases associated with WT1 expression, e.g. leukemia (especially acute/chronic myeloid leukemia primers, used in the exemplification of the present invention.</pre>
<pre>XX XX XX Mouse: Wilns' tumour; WT1; pleural mesothelioma; antigen; KW acute lymphocytic leukaemia; ALL; myeLodysplastic syndromes; myeloproliferative syndrome; cancer; cytostatic. XX Mus musculus. XX W0200162920-A2. XX V0200162920-A2. XX 20-AUG-2001. 22-FEB-2001; 2001WO-US05702. PF 22-FEB-2000; 2000US-184070P. XX (CORI-) CORIXA CORP. XX Cheever MA, Gaiger A; XX WPI; 2001-648218/74. XX Composition for the treatment of mesothelioma comprises specific PF peptides i.e. Wilms' tumour antigen polypeptide derived antigenic. XX Claim 1; Page 24; 242pp; English. XX XX XX XX XX XX XX XX XX X</pre>	ARUGB802 ID AAUG8602 standard; Peptide; 23 AA. XX AAUG8602; AC AAUG8602; XX DT 16-JAN-2002 (first entry) DT 16-JAN-2002 (first entry) XX DT 16-JAN-2002 (first entry) XX DT 16-JAN-2002 (first entry)	<pre>XX XX PT Cheever MA, Gaiger A; XX WPI; 2001-648218/74. XX XX Composition for the treatment of mesothelioma comprises specific pr fragments - Wilms' tumour antigen polypeptide derived antigenic fragments - Wilms' tumour antigen polypeptide derived antigenic fragments - Vilms' tumour prospection comprising at least a CC first isolated peptide, of between 9 and 40 amino acids or a first nucleic acid, enoding the peptide, in the manufacture of a medicament CC peptides derived from the Wilms' tumour, preferably CC petides derived from the Wilms' tumour preferably CC petides derived from the Milms' tumour preferably CC petides derived from the prescheliona. ALL, and childhood ALLL, CC myelodysplastic syndromes, myeloproliferative syndromes and cancers preferably humans. The present sequence is an antigenic peptide of the invention derived from human WTI. So Sequence 23 AA; Ouery Matches 9; Cconservative 0; Mismatches 0; Indels 0; Gaps 0 V 1 INFPNAPYL 9 1011111111 10 RMFPNAPYL 18 DD 10 RMFPNAPYL 18</pre>

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Page 8

QY Query Match 100.0%; score 51; DB 22; Length 23; Best Local Similarity 100.0%; Pred. No. 0.006; Matches 9; Conservative 0; Mismatches 0; Indels ( The invention relates to the use of a composition comprising at least a first isolated peptide, of between 9 and 40 amino acids or a first nucleic acid, encoding the peptide, in the manufacture of a medicament for treating or preventing mesothelioma. The peptides are antigenic peptides derived from the Wilms' tumour protein WT1. The composition is useful for the treatment of mesothelioma. The peptides e.g. leukaemia (including acute myeloid leukaemia, AML, chronic myeloid leukaemia, including acute lymphocytic leukaemia, ALL, and childhood ALL), myelodysplastic syndromes, myeloproliferative syndromes and cancers (e.g. breast, testicular, present sequence is an antigenic peptide of the invention derived from mouse WT1. Sequence 1 RMFPNAPYL 9 |||||||| 10.RMFPNAPYL 18 23 AA; <u>,</u> Gaps <u>,</u>

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<pre>by non-profit institutions as long as its content is in no way ied and this statement is not removed. Usage by and for commercial ies requires a license agreement (See http://www.isb-sib.ch/announce/ nd an email to license@isb-sib.ch). x69716; CAA49373.1; p08046; laAx rAC; T02352; . Pro: IPR000976; wilms_tumour. pro: IPR000976; zif-C2H2; 4. pr00056; zif-C2H2; 4. pr00065; zif-C2H2; 2. s; PR00048; ZINC_FINGER_C2H2_1; 4. TE: PS0057; ZINC_FINGER_C2H2_1; 4. TE: PS0057; ZINC_FINGER_C2H2_2; 4. finger; Metal-binding; DNA-binding; Repeat; Nuclear protein; cription regulation; Alternative splicing; Anti-oncogene. N 227 837 ZINC FINGERS.</pre>	ELLUL RNATI RNATI UCEd SPI UCPME LOP	<pre>Metazoa; (Rat). Metazoa; Chordata; Craniata; Vertebrata;   utheria; Rodentia; Sciurognathi; Muridae; 10116; 00M N.A. gue-Dawley; TISSUE-Kidney; gue-Dawley; TISSUE-Kidney; 46155; PubMed=1330293; , Yang X., Bowman M., Roberts V., Sukumar cloning of rat Wilms' tumor complementary cloning of rat Wilms' tumor complementary 52:6407-6412(1992). 52:6407-6412(1992).</pre>	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	36       70.6       487       1       C8B1_ESCCA         36       70.6       488       1       C8B2_ESCCA         36       70.6       509       1       C4A1_DROME         36       70.6       618       1       TRX6_ANGCA         35       68.6       273       1       TRX6_ANGCA         35       68.6       273       1       TPSA_CAREL         35       68.6       203       1       TPSA_CAREL         35       68.6       500       1       C912_ARATH         34       66.7       180       1       YH95_AQUAE         34       66.7       1097       1       STRMU         33       64.7       1097       1       CCT_DROME         33       64.7       110       1       YLXM_STRMU

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database."; VARIANTS DMS TYR-3 MEDLINE=98198341; Nat. "The 01) Hum 'n Little M.H., Williamson K.A., Hastie N.D., van Heyningen V. "Evidence that WT1 mutations MEDLINE=93271983; PubMed=8388765; Little M.H., Williamson K.A., Man Nat. Hum. "Constitutional mutations MEDLINE=93265053; PubMed=1338906; Baird P.N., Santos A., Groves N., Cell Rauscher F.J. 1 "The WT1 Wilms REVIEW REVIEW VARIANTS tissues MEDLINE=94004972; VARIANT VARIANTS DDS SEQUENCE OF Denys-Drash syndrome. VARIANTS syndrome MEDLINE=92005721; PubMed=1655284; Pelletier J., Bruening W., Kashta VARIANTS MEDLINE=93345769; 14 [12 11 MEDLINE=93250986; 8 μ solated diffuse mesangial ۵ ч • Biol. dence that WT1 mutations in D
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Mo1. Genet. 2:259-264(1993). Mol. Genet. 67:437-447(1991). Hum. .A., Buckler A.J.; novel tumor suppressor 1. 4:97-106(1992). MESOTHELIOMA GLY-273. -94004972; PubMed=8401592; WT DDS DDS SER-181 AND ALA-253 385-405 FROM Genet. TYR:377; III; factor tumor 1:301-305(1992). PubMed=9529364; namur E., Henry PubMed=1302008; PubMed=8393820; PubMed=1313285; gene in th Groves N., ions in the N.A.,

Jeanpierre C., Denamur E., Henry I., Cabanis M.-Cecille A., Elion J., Peuchmaur M., Loirat C., N Gubler M.-C., Junien C.; "Identification of constitutional WT1 mutations, "Identification of constitutional WT1 mutations, Park S., Schalling M., Bernard A., Ma Roberts D., Fletcher J., Shipman R., Griffin J., Minden M., Housman D.E., Bruening W., Bardeesy N., Silverman B.L., Aronson A.J., Housman D., Pelletier J.; "Germline intronic and exonic mutations in (WT1) affecting urogenital development."; Nat. Genet. 1:144-148(1992). MEDLINE=97268681; PubMed=9108089; Schumacher V., Schneider S., Figge A., Wildhardt G., Harms D., Schmidt D., Weirich A., Ludwig R., Royer-Pokora B.; "Correlation of germ-line mutations and two-hit inactivation o WT1 gene with Wilms tumors of stromal-predominant histology."; Proc. Natl. Acad. Sci. U.S.A. 94:3972-3977(1997). associated with abnormal urogenital development syndrome.": Pelletier J., Bruening W., Kashtan C.E., Mauer S.M. Striegel J.E., Houghton D.C., Junien C., Habib R., Fine R.N., Silverman B.L., Haber D.A., Housman D.; "Germline mutations in the Wilms' tumor suppressor Lis D., Fletcher J., Shipman R., Rheinwald J., Gin J., Minden M., Housman D.E., Haber D.A.; Wilms tumour gene WT1 is expressed in murine ues and mutated in a human mesothelioma."; Genet. 4:415-420(1993). 62:824-833(1998). esangial sclerosis, correlations by us LEU-383 AND ASN-396 ne product: a dev the kidney that Mannens gene AND λq Denys-Drash WT1 use Jadresic VARIANT inactivated gene developmentally regulated hat functions as a tumor and М., 0f 5 analysis of a computeri Cohn 5 Kelsey ٢. the DDS computerized syndrome patients D.; F Niaudet Wilms' tumour R.A., Machin **TRP-394** Cowell ; ; ij ĺ'n 'n Shipley G , Demetri A., mesoderm-derived Wilms' gene are Denys-Drash Luce S det P., Fouser patients patients may Gosden Manivel J.K.; with S mutation G.C., tumor."; Г., G:, G.A., C of J.C., with gene the act

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PRINTS; PR00049; WILMSTUMOUR. PRINTS; PR000048; ZINCFINGER. ProDom: PD000003; ZnF\_C2H2; 2. SMART; SM00355; ZnF\_C2H2; 4. SMART; SM00355; ZINC\_FINGER\_C2H2\_1; 4. PROSITE; PS00128; ZINC\_FINGER\_C2H2\_2; 4. Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein; Transcription regulation; Alternative splicing; Anti-oncogene; MIM; MIM; TRANSFAC; TRANSFAC; EMBL; EMBL; Disease mutation. DOMAIN 27 MIM HSSP; P08046; 1AAY. TRANSFAC; T00899; -. TRANSFAC; T00900; -. EMBL; EMBL; Pfam; Pfam; PIR; A34673; A34673. PIR; S08273; S08273. EMBL; EMBL; EMBL; the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com This FASEB InterPro; Genew; TRANSFAC ; EMBL; EMBL; EMBL; EMBL; ç entities ÷ DOMAIN InterPro; IPR000976; TRANSFAC; EMBL; EMBL; between ÷ ÷ .<u>+</u> ÷ send an email to license@isb-sib.ch). genital abnormalities. DISEASE: Defects in WT1 are the cause of diffuse mesangial sclerosis (DMS), a form of Denys-Drash syndrome. SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER EB J. 7:896-903(1993). FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCCGC-3'. SUBCELLULAR LOCATION: Nuclear. SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; are produced by alternative splicing. TISSUE SPECIFICITY: EXPRESSED IN THE KIDNEY AND A SUBSET OF DISEASE: Defects in WT1 are a cause embryonal malignancy of the kidney t 10'000 infants and young children. 1 DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infoblogen.fr/services/chromcancer/Genes/WT1ID78.html" DATABASE: NAME=WT1; NOTE=WT1 mutation database; WWW="http://www.und.necker.fr:2003/". PROTEINS. DISEASE : 256370; hereditary forms. HEMATOPOIETIC CELLS 194070; SWISS-PROT entry is copyright. It is produced through a collaboration -een the Swiss Institute of Bioinformatics and the EMBL outstation -(DDS), 194080; -. PF00096; zf-C2H2; 4. PF02165; WT1; 1. M80232; M80217; S6151 M80219; S60755; M30393; M80231; M802 M80220; M80218; X51630; HGNC:1 ; T01841; -. ; T01842; -. GNC:12796; WT ; T01839; -. ; T01840; -. requires a license agreement (See http://www.isb-sib.ch/announce/ IPR000822; E: Defects in WT1 are the cause of Denys-Drash syndrome a disease characterized by a typical nephropathy and 27 ; AAA61299.1; AAA61299.1; AAA61299.1; AAA61299.1; AAA61299.1; AAA61299.1; ; CAA35956.1; ; AAA61299.1; ; AAA61299.1; AAB20110. AAC60605. AAA61299. AAA61299 AAA61299 AAA61299 ,**'** WT 83 438 Wilms\_tumour Znf\_C2H2 . . . . <u>.</u> ÷ JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. ALT\_INIT .' .' .' PRO-RICH. ZINC FINGERS ЪХ Ð e of Wilm's tumor (WT), an that affects approximately It occurs both in sporadic typical nephropathy for and commercia. 1 in and on no way its ŧ B Q

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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4. PROSITE; PS00028; ZINC_FINGER_C2H2_2; 4. Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein; Transcription regulation; Alternative splicing; Anti-oncogene. DOMAIN 28 83 ZINC_FINGERS. ZN_FING 323 347 C2H2-TYPE. ZN_FING 353 377 C2H2-TYPE. ZN_FING 383 405 C2H2-TYPE. ZN_FING 383 405 C2H2-TYPE. ZN_FING 383 405 C2H2-TYPE. ZN_FING 344 265 MISSING (IN ISOFORM 2 AND ISOFORM 3) (BY VARSPLIC 407 409 MISSING (IN ISOFORM 2 AND ISOFORM 4) (BY	EMBL; ABU10959; BAA28147.1; HSSP; P08046; IAAX. InterPro; IPR000976; Wilms_tumour. InterPro; IPR000822; Znf_C2H2. Pfam; PF000956; Zf-C2H2; 4. Pfam; PF020465; WTL; 1. Pfam; PF02046; WILKSTUMOUR. PRINTS; PR00046; ZINCFINGER. PRINTS; PR00046; ZINCFINGER. PRINTS; PR00046; ZINCFINGER. PRINTS; PR00046; ZINCFINGER.	entry is cop iss Institute Dinformatics Difit Institute is statement is statement a license l to license	<pre>SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-LWD; TISSUE-Kidney; MEDLINE-98267201; pubMed=9602131; TSUTULANI N. Oda H., NakatSUTU Y., Imai Y., Zhang S., Ueno Y., IShikawa T.; "CDNA cloning and developmental expression of the porcine homologue of WT1.";125-220(1998). -!- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCGCC3'. -!- SUBCELLULAR LOCATION: Nuclear. -!- SUBCELLULAR LOCATION: Nuclear. -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; may be produced by alternative splicing. -!- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT. -!- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.</pre>	SULT 4 1_PIG STANDARD; PRT; 449 AA. 062651: 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 47, Last sequence update) 15-JUR-2002 (Rel. 41, Last annotation update) Wilms' tumor protein homolog. WT1. Sus Scrofa (Pig). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. NCBI_TAXID=9823; [1]	<pre>2 SEQUENCE 449 AA; 49246 MW; 962381E9C8D7A380 CRC64; Cuery Match 100.0%; Score 51; DB 1; Length 449; Best Local Similarity 100.0%; Pred. No. 0.025; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 RMFPNAPYL 9 1               5 126 RMFPNAPYL 134</pre>
EMBL; TIGR; InterF Pfam; Membra SIGNAL CHAIN LIPID SEQUEN SEQUEN Matches	CC		[1] SEQU MEDL Flei Kerl Weid Utte Gnet Yent Yent	RESULT 5 VFTO_HAEIN STANDARD; PRT; 262 AA. AC P44553; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DE Putative lipoprotein HI0177 precursor. GN HI0177. OS Haemophilus influenzae. OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; OX MCBH TaxID=727.	<pre>FT SQ SEQUENCE 449 AA; 49166 MW; 9C3E557B96F5A7B3 CRC64; Ouery Match 100.0%; Score 51; DB 1; Length 449; Best Local Similarity 100.0%; Pred. No. 0.025; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 1 RMFPNAPYL 9 0; 126 RMFPNAPYL 134</pre>

RESULT UN33\_C7 UN AC Q0 DT 01 DT 01 DT 12 DT 12 CR UT CS C2 RESULT IFT2\_CH 망 Q 망 QY #2\_CRLU # IFT2\_CRILO Concernment 1 000462; T 001-NOV-1997 (Rel. 35, Created) T 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) Thereferon-induced protein with tetratricopeptide repeats 2 ( Thereferon-induced 54 kDa protein) (IFI-54K) (CL-54 K). Thereferon-induced 54 kDa protein) (IFI-54K) (Chinese hams Thereferon induced 54 kDa protein) (IFI-54K) (Chinese hams Therefore induced 54 kDa protein) (CHINESE hams) (CHINESE hams) (CHINESE hams) (CHINESE hams) (CHINESE hams) (CHINESE Query Match Best Local S Matches ( UN33\_CAEEL STANDARD; 001630; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last seq 15-JUN-2002 (Rel. 41, Last ann 15-JUN-2012 (Rel. 41, Last ann) REPEAT SEQUENCE Caenorhabditis elegans Uncoordinated CAEEL REPEAT Repeat; REPEAT use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). This Eur. Bluyssen J.A.R., Vlietstra R.J., van der Made A., Trapman J.: "The interferon-stimulated gene 54 K promoter contains two adjacent functional interferon-stimulated response elements of different strength, which act synergistically for maximal interferon-alpha **UNC-33** Pfam; PF00515; EMBL; X77259; CAA54477.1; -. the European Bioinformatics Institute. SEQUENCE FROM N.A. NCBI\_TaxID=10030; Cricetulus Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster) REPEAT REPEAT between ÷ MEDLINE=94170787; PubMed=8125096; ÷ inducibility."; 203 nterPro; 151 7 თ 4 н Ч INDUCTION: BY INTERFERONS. SIMILARITY: BELONGS TO THE IFIT FAMILY. SIMILARITY: CONTAINS 6 TPR REPEATS. || ||:||: RMSPNSPYV 211 RMFPNAPYL 9 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN <u>-</u> **RVFPNSPY 158** RMFPNAPY Similarity 6; Conserv Biochem. 220:395-402(1994). TPR repeat; ......... IPR001440; 364 468 AA; 94 138 175 242 327 Conservative protein ω TPR; 127 208 275 360 398 4 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Cricetinae; 55045 Interferon 72.5%; 66.7%; TPR. Last sequence update) Last annotation updat 33 (Protein unc-33). MW; 2 Score 37; Pred. No. TPR TPR TPR TPR TPR TPR PRT; induction 9D92B878F81B1E27 CRC64; Mismatches  $\omega \sim \mu$ **4 Ν Ο** 854 update) DB 12; There are no rest ong as its content ΑA 1; н ;; Length 468, Indels restrictions EMBL outstation 2 (IFIT-2) a collaboration 0; Gaps 0 its 0;

RESULT 8 BIR1\_HUMAN 망 Qy Query Match Best Local Matches EMBL; Z14148; CAA78520.1; -EMBL; Z14148; CAA78521.1; -EMBL; Z14148; CAA78522.1; -EMBL; Z14146; CAA78516.1; -EMBL; Z14146; CAA78517.1; -EMBL; Z14146; CAA78517.1; -BIR1\_HUMAN STANDARD; PRT; 1403 AA. Q13075; Q13730; Q99796; O75857; O1-NOV-1997 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis Roy N., Mahadevan M.S., McLean M., Shut Farahini R., Baird S., Besner-Johnston Salih M., Aubry H., Tamai K., Guan X., Eukaryota; Metazoa; Mammalia; Eutheria; This TISSUE=Fetal brain; MEDLINE=95112344; PubMed=7813013; SEQUENCE FROM inhibitory protein). BIRC1 OR NAIP. PIR; PIR; entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. ÷ -i- FUNCTION: INVOLVED IN AXONAL GUIDANCE AND OUTGROWT -i- SUBCELLULAR LOCATION: Cytoplasmic. -i- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), gene unc-33. NCBI\_TaxID=9606; Homo sapiens (Human) SEQUENCE VARSPLIC Alternative PIR; between -!- SIMILARITY: BELONGS TO THE DEHYDROPYRIMIDINASE FAMILY. Genetics 132:675-689(1992). STRAIN=Bristol N2; MEDLINE=93106371; PubMed=1468626; Li W., Herman R.K., Shaw J.E.; "Analysis of the Caenorhabditis elegans axonal Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. VARSPLIC Pfam; PF00744; Dihydroorotase; SEQUENCE FROM NCBI\_TaxID=6239; inhibitory InterPro; 773 μ and 3/55.5 kDa; may be produced by alternative splicing. DEVELOPMENTAL STAGE: UNC-33 PROTEINS ARE DISTRIBUTED EXCLUSIVELY WITHIN NEURONAL PROCESSES AFTER EARLY EMBRYOGENESIS. \$24643; \$24643. \$24644; \$24644. \$33558; \$33558; rÞro; IPR002195; Dihydrooratase. SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN RLSPNSPYL 781 RMFPNAPYL 6 ; Similarity 854 AA; splicing = Conservative I N.A. N.A. μ 9 331 Chordata; Primates; 175 90819 MW; 72.58; 66.78; ...... 2 MISSING (IN ISOFORM Pred. Score 37; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. A8073DDE251D2D77 CRC64; ÷ Mismatches Shutler G., Yaraghi Z., ston A., Lefebvre C., Ka X., Ioannou P., Crawfo No. 22; There are no rest ng as its content DB 1; Usage 1; OUTGROWTH Length 854 guidance  $\omega \omega$ Indels Crawford рÀ restrictions 2/72.1and and Kang EMBL st Q l T.O., 0; for outgrowth collaboration kDa outstation 5 Gaps commercia ŋ g way its 0 ,

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<pre>EMBL; U19251; AAC52045.1; EMBL; U20017; AAC52047.1; EMBL; U21913; AAA64504.1; EMBL; AC005031; AAA64504.1; HSSP; Q13490; 1QBH. Genew; HGNC:7654; BIRC1. MIM; 600355; InterPro; IPR001370; BIR. PFAm; PF00653; BIR; 3. PROSITE; PS01282; BIR_REPEAT_1; 3. PROSITE; PS01282; BIR_REPEAT_2; 3. PROSITE; PS012837; NACHT; 1. Apoptos1s2; Repeat. Apoptos1s2; Repeat. Apoptos1; Repeat. Apoptos1; Repeat. Apoptos1; Repeat. Apoptos1; Repeat. Apoptos1; Repeat. Apoptos1; Repeat. Apopto</pre>	NEWBORNS. ( - :- SIMILARITY: CONTAINS 3 BIR REPEATS. - :- SIMILARITY: CONTAINS 1 NACHT DOMAIN. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the_EMBL contractions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@isb-sib.ch).	<ul> <li>-1. TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN SPINAL CORD.</li> <li>-1. DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE 1). SMAS ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1 (WEDNOIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE III (WOHLFART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO PROGRESSIVE PARALYSIS MUSCILIAR ATROPHY. CONCERNS 1 N 6000</li> </ul>	he EMBL/GenBank/DDBJ databases. N.A. erson J.; he EMBL/GenBank/DDBJ databases. he EMBL/GenBank/	<pre>de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.; "The gene for neuronal apoptosis inhibitory protein is partially deleted in individuals with spinal muscular atrophy."; [2] SEQUENCE FROM N.A., AND REVISIONS TISSUE-Brain; MEDLINE-99163755; PubMed=9503025; Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R., Xuan JY., Kang X., Lefebvre C., Ikeda JE., Korneluk R.G., MacKenzie A.E.; "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular atrophy candidate genes SIM and NAIP."; [3] SEOUENCE OF 386-623 FROM N.A. der Steege G. Draaijers T.G., Grootscholten P.M., Osinga J., Anzevino R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,</pre>
<pre>RA Comstock K.E., Sanderson B.J.S., Claflin G., Henner W.D.; RA Comstock K.E., Sanderson B.J.S., Claflin G., Henner W.D.; RT "GST1 gene deletion determined by polymerase chain reaction."; RL Mucleic Acids Res. 18:3670-3670(1990) RP SEQUENCE OF 1-23. RA MEDLINE=86042634; PubMed=3864155; RA Mannervik B., Alin P., Guthenberg C., Jensson H., Tahir M.K., RA Mannervik B., Alin P., Guthenberg C., Jensson H., Tahir M.K., RA Mannervik B., Alin P., Guthenberg C. Jensson H., Tahir M.K., RA Marholm M., Joernvall H.; RT 'Identification of three classes of cytosolic glutathione transferase RT common to several mammalian species: correlation between structural RT data and enzymatic properties."; RT REQUENCE OF 1-23. RE Proc. Natl. Acad. sci. U.S.A. 82:7202-7206(1985). RE MEDLINE=85154554; PubMed=3979555;</pre>			RESULT 9 GTM1_HUMAN STANDARD; PRT; 217 AA. AC P09488; DT 01-FEB-1989 (Rel. 10, Created) DT 01-FEB-1991 (Rel. 17, Last sequence update) DT 01-FEB-1991 (Rel. 17, Last sequence update) DE Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GSTM1-1) (HB subunit 4) DE Glutathione S-transferase (Rel. 19, CSTM1-1) (GST class-mu 1). GN GSTM1 OR GST1. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. N (D1-TaxID-9606; DM (D1-TaxID-9606;	<pre>FT REPEAT 159 227 BIR 2. FT REPEAT 278 345 BIR 3. FT DOMAIN 464 758 NACHT. FT CONFLICT 222 723 PF -&gt; YR (IN REF. 4). FT CONFLICT 386 387 VP -&gt; ST (IN REF. 3). FT CONFLICT 535 535 V -&gt; V (IN REF. 3). FT CONFLICT 1228 1231 MISSING (IN REF. 3). FT CONFLICT 1228 1231 MISSING (IN REF. 4). SQ SEQUENCE 1403 AA; 159613 MW; 566304C154DA5E64 CRC64; Duery Match 72.5%; Score 37; DB 1; Length 1403; Best Local Similarity 66.7%; Pred. No. 38; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gáps [] NHFPNAPYL 9 []       1:1 Db 337 RCFPNCPFL 345</pre>

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RESULT 10 GTM1\_MOUSE QY Query Match Best Local Matches CONFLICT This SWI between the Euro Patskovsky Y.V., Patskovska L.N., Listowsky I.; "Functions of His107 in the catalytic mechanism of human g s-transferase hGSTM1a-1a."; Biochemistry 38:1193-1202(1999). i FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. .i - CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutat PIR; PIR; EMBL; "Structural evidence for three transferase in human tissues."; FEBS Lett. 182:319-322(1985). Pfam; PF00043; GST\_C; Pfam; PF02798; GST\_N; PRINTS; PR01267; GSTRN PDB; PIR; EMBL; EMBL; ÷÷ Hubbard M.J., McHugh N.J.; "Human ERp29: Isolation, primary structural characterisation two-dimensional gel mapping."; Electrophoresis 21:3785-3796(2000). MUTAGEN VARIANT INIT\_ Transferase; InterPro; IPR004046; GST\_Cterm InterPro; IPR004045; GST\_Nterm InterPro; IPR003081; GST\_mu. MIM; Genew; EMBL; entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). modified use <u>.</u> ÷ + ÷ MEDLINE=99130249; X-RAY CRYSTALLOGRAPHY (2.68 ANGSTROMS), MEDLINE=21088920; TISSUE=Liver; SEQUENCE OF 52-59, AND MASS SPECTROMETRY 8 56 E: ω LL; X08020; CAA30821.1; Ll; X08820; CAA459203.1; LL; X68676; CCAA46536.1; LL; X51451; CAA35817.1; L; X51451; CAA35817.1; L; 22457; B22457. L; B22457; B22457. L; B22457; B22457. L; B22457; B22457. s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest MET SIMILARITY: BELONGS TO THE GST SUBCELLULAR LOCATION: Cytoplasmic. TISSUE SPECIFICITY: THIS IS A LIVER ISOZYME POLYMORPHISM: THERE ARE TWO ALLELES; GSTMIA SUBUNIT: HOMODIMER. DIFFER IN POSITION 172. Р., 138350; FPNLPYL FPNAPYL 1GTU; 02-FEB-99 ğ HGNC:4632; Similarity 6; Conser non-profit institutions as long a and this statement is not removed. requires a license agreement (See ] Mannervik B., 43 217 1 Multigene 0 0 Conservative 107 172 62 ە AA; GSTRNSFRASEM. GSTM1 PubMed=9930979; PubMed=11271497; 172 107 43 25580 70 85 for three different types family; Joernvall H.; .68; .78; '\_Nterm . . . .' MW; 0 Score Pred. /FTId=VAR\_003617. H->S: CHANGE THE PROPERTIES TOWARD SOME SUBSTRATES. S -> T (IN REF 3). ㅈ -> T (IN REF. 3) A8BB0E713BA75EAB Polymorphism; v Mismatches N (IN ALLELE d=VAR 003617. 36; I SUPERFAMILY. MU There are no rest ng as its content AND DB 7.7; <u>.</u> MUTAGENESIS 3D-structure Usage 1; в) . Length 217 of glutathione CRC64; AND Indels FAMILY. Уq -glutathione GSTM1B restrictions WIDE NUMBER and OF OF glutathione EMBL is a collaboration WHICH HIS-107 0; THE for and outstation h Gaps ENZMYE commercia no g way its 0 01-JUL-1989 (Rel. 11, Creater, 01-JUL-1989 (Rel. 11, Last sequence update) 15-JUL-1989 (Rel. 11, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Glutathione S-transferase Mu 1 (EC 2.5.1.18) modification of murine glutathione S-transferases."; Chem. Res. Toxicol. 8:1054-1062(1995). -:- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBE OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. -:- CATALYIC ACTIVITY: RX + glutathione = HX + R-S-glutathione. STRAIN-CD-1; TISSUE-Liver; STRAIN-CD-1; TISSUE-Liver; MEDLINE=96189427; PubMed=8605288; Mitchell A.E., Morin D., Lame M.W., Jones A.D.; "Purification, mass spectrometric characterization, "Purification, mass spectrometric characterization, " MEDLINE=90094327; PubMed=2689439; Townsend A.J., Goldsmith M.E., Pickett C.B., Cowan K.H.; "Isolation, characterization, and expression in Escherichia coli of two murine Mu class glutathione S-transferase cDNAs homologous to t rat subunits 3 (Yb1) and 4 (Yb2)."; J. Biol. Chem. 264:21582-21590(1989). data Pearson W.R., Windle J.J., Morrow J.F., "Increased synthesis of glutathione S-t: anticarcinogenic antioxidants. Cloning i "The structure of two murine class-mu glutathione coordinately induced by butylated hydroxyanisole." Arch. Biochem. Biophys. 303:383-393(1993). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; This SWISS-PROT entry -!- SUBUNIT: HOMODIMER.
 -!- SUBCELLULAR LOCATION: Cytoplasmic.
 -!- MASS SPECTROMETRY: MW=25838.4; MW\_ERR=2; METHOD=Electrospray
 -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY. Proc. Natl. "Identification of three classes Mannervik B., Alin P., Gu Warholm M., Joernvall H.; PRELIMINARY SEQUENCE OF 1-24. MEDLINE=86042634; PubMed=3864155; RNA. SEQUENCE FROM N.A. MEDLINE=93290350; SEQUENCE FROM butylated MEDLINE-88330838; PubMed-3417659; Pearson W.R., Reinhart J., Sisk S.C., "Tissue-specific induction of murine MEDLINE=88330838; NCBI\_TaxID=10090; between CHARACTERIZATION common MEDLINE=83109018; PRELIMINARY SEQUENCE OF 1-40 Submitted Strausberg SEQUENCE Reinhart J., Pearson W.R.; Mus musculus P10649; GTM1\_MOUSE 6 ნ ω 2 Biol. Biol. and to several mammalian species: correlation nd enzymatic properties."; Natl. Acad. Sci. U.S.A. 82:7202-7206(1985). FROM Chem. 258:2052-2062(1983). the Chem hydroxyanisole."; Chem. 263:13324-13332(1988). (FEB-2001) to Swiss (Mouse) N.A. N.A. STANDARD; PubMed=6822548; PubMed=8512323; Institute is copyright. stitute of Bio Guthenberg the EMBL/GenBank/DDBJ Craniata; Vertebrata; Sciurognathi; Muridae, PRT; ght. It is produced through Bioinformatics and the EM of с., 2 2.5.1.18) (GST class-mu (pmGT10) (GST 1-1). cytosolic .F., Benson A.M., S-transferases 1 , Anderson K glutathione 217 Jensson H., and ₿ measurement Muridae; glutathione transferase cDNAs homologous to the databases between structural transferase ŝ Tahir M. transferase in response nent of messe and Euteleostomi; Talalay P.; Adler P Murinae; covalent EMBL ~ messenger a collaboration NUMBER 5 z mRNAs Mus. outstation genes 5 ЪУ

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	<pre>RP SEQUENCE FROM N.A. (CLONE PGTA/C44). RX MEDLINE=66037768; PubMed=3840477; RA Ding G.JF., Lu A.Y.H., Pickett C.B.; RT "Rat liver glutathione S-transferases. Nucleotide sequence analysis RT of a Yb1 cDNA clone and prediction of the complete amino acid RT sequence of the Yb1 subunit."; RL J. Biol. Chem. 260:13268-13271(1985). RN [3]</pre>				RESULT 11 GTM1_RAT ID GTM1_RAT STANDARD; PRT; 217 AA. AC P04905:	Qy 3 FPNAPYL 9 111 111 Db 56 FPNLPYL 62	Query Match 70.6%; Score 36; DB 1; Length 217; Best Local Similarity 85.7%; Pred. No. 7.7; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		DR InterPro; IPR004046; GST_Cterm. DR InterPro; IPR004045; GST_Nterm. DR InterPro; IPR003081; GST_mu. DR Pfam; PF00043; GST_C; 1. DR Pfam; PF02798; GST_N; 1.				CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch).
PIR	CC -i- SIMILARITY: BELONGS TO THE GST SU CC This SWISS-PROT entry is copyright. I CC between the Swiss Institute of Bioin CC the European Bioinformatics Institute CC use by non-profit institutions as CC modified and this statement is not re CC entities requires a license agreement	• • • • • •	RL Biochemistry 33:1043-1052(1994). CC -i- FUNCTION: CONJUGATION OF REDUCED CC -i- FUNCTION: THE OLFACTORY GST MAY B CC -I- FUNCTION: THE OLFACTORY GST MAY B	പതന്ത്രം പാലം		RN [8] RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) RA Fu JH., Rose J., Tam M.F., Wang B RT "New crystal forms of a mu-class glut RT liver.";	RT The three-dimensional structure of a RT the mu gene class. Structural analysi RT isoenzyme 3-3 and glutathione at 2.2- RL Biochemistry 31:10169-10184(1992).	Biochem. J. 278:293-297(1991). [7] X-RAY CRYSTALLOGRAPHY (2.2 ANGST MEDLINE-93041702; PubMed-1420139 MEDLINE-93041702; AND	MUTAGENESIS MEDLINE=9135 Hsieh JC., "Cysteine-86 transferase	RA Ben-Arie N., Khen M., Lancet D.; RT "Glutathione S-transferases in rat ol RT purification, molecular properties an RL Biochem. J. 292:379-384(1993). RN [6]	( 5 ) SEQ MED	RT androgen-repressed mRNA by cDNA cloni RT J. Biol. Chem. 262:11901-11903(1987).	RT phenobarbital."; RL J. Biol. Chem. 261:7952-7957(1986). RN [4] RP SEQUENCE FROM N.A. RX MEDLINE-87308179; PubMed=3040722; RA Chang C Saltzman A.G. Sorensen N

(8: W.-L., Lai Y.-C., Tam M.F.; the enzymic activity of glutathione sght. It is produced through a collaboration Bioinformatics and the EMBL outstation -titutute. There are no restrictions on its ons as long as its content is in no way not removed. Usage by and for commercial "eement (See http://www.isb-sib.ch/announce/ -sib.ch). Lasmic. UTATHHONE S-TRANSFERASES (GST) CONSIST HREE MAJOR CLASSES OF SUBUNITS (27 KDA) AND YC (28 KDA). SELECTIVELY BINDS STEROID HORMONES. GST SUPERFAMILY. MU FAMILY. ;TROMS). ing B.-C.; is glutathione S-transferase from rat 22; sen N.S., Hilpakka R.A., Liao S.; S-transferase Ybl mRNA as the A cloning and sequence analysis."; (1987). , Gilliland G.L.; e of a glutathione S-transferase from nalysis of the binary complex of t 2.2-A resolution."; cepithelium; 3; DUCED GLUTATHIONE TO A WIDE NUMBER HYDROPHOBIC ELECTROPHILES. MAY BE CRUCIAL FOR THE ACUITY OF THE xenobiotic substrate binding site of a vealed by X-ray crystallographic ith the diastereomers of 9-(S-ihydrophenanthrene."; 2). 2 2 utathione - HX + R-S-glutathione. (ROMS). 1994). FROMS). rat olfactory epithelium: ies and odorant biotransformation."; Dickert L., Prasad S.M., Ammon H.L., ...... .....

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RESULT 12 GTM2\_HUMAN ID GTM2\_HI AC P28161 DT 01-APR DT 01-APR 炅 QY Query Match Best Local S Matches 6 GTM2\_HUMAN STANDARD; PRT; 217 AA P28161; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) HELIX TURN HELIX TURN TURN TURN STRAND TURN STRAND TURN STRAND TURN STRAND TURN INIT\_MET MUTAGEN PDB; PDB; TURN HELIX TURN HELIX TURN TURN HELIX HELIX TURN HELIX TURN Pfam; PF00043; GST\_C; Pfam; PF02798; GST\_N; PRINTS; PR01267; GSTRN PDB; PDB; SEQUENCE PDB; PDB; CONFLICT PDB; PDB; PDB; PDB; PDB; HELIX HELIX CONFLICI Transferase; Multigene InterPro; InterPro; InterPro; PDB; PDB; PIR; 56 3 FPNAPYL 9 : A25510; A25510. : A29794; A29794. : S17167; S17167. 16SC; 26ST; 36ST; 56ST; 56SST; 66SST; 66SSV; 66SSV; 5FWG; FPNLPYL 62 1GSB; Similarity 85. 6; Conservative IPR004045; GST\_Nterm. IPR003081; GST\_mu. IPR004046; 08 - NON - 80 96 - NON - 80  $\frac{210}{217}$ 27 - JAN - 99 96-AON-80 96 - AON - 80 08-VOV-96 96-AON-80 31-OCT-93 31-OCT-93 31-JAN-94 31-OCT-93 31-OCT-93 31-OCT-93 197 142 154 155 171 115 117 168 189 191 178 130 119 129 AA; GSTRNSFRASEM 1111 1111887665433221 11118876640622423 1254228 0 86 168 199 188 196 196 201 211 70.6%; 85.7%; 25782 MW; GST\_Cterm family; Score 36; DB Pred. No. 7.7; 0; Mismatches <u>,</u> C->S: NO CHANGE I -> N (IN REF. KS -> NC (IN REF 2ACE8D49DA785118 CRC64; 3D-structure; Olfaction. -> NC (IN REF. 2). DB 1; Length 217; AA IN ACTIVITY 3). <u>ب</u> Indels 0; Gaps <u>,</u> STRAND TURN STRAND HELIX TURN STRAND TURN STRAND HELIX TURN HELIX TURN STRAND SEQUENCE room, .... MEDLINE-91239584; PubMed=2034681; Vorachek W.R., Pearson W.R., Rule G.S.; "Cloning, expression, and characterization of a class-mu glutathione transferase from human muscle, the product of the GST4 locus."; prnc. Natl. Acad. Sci. U.S.A. 88:4443-4447(1991). STRAND TURN InterPro; IPR004046; GST\_Cterm. InterPro; IPR004045; GST\_Nterm. InterPro; IPR003081; GST\_mu. Pfam: PF00043; GST\_C; 1. Pfam; PF02798; GST\_N; PRINTS; PR01267; GSTRN PDB; PDB; PDB; PDB; PDB; PIR; use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ This -!- SUBCELLULAR LOCATION: Cytoplasmic. -!- TISSUE SPECIFICITY: THIS IS A MUSCLE ISOZYME. -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY. OF EXCGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione. "Crystal structure of human class mu glutathione transferase GSTM2-2. Effects of lattice packing on conformational heterogeneity."; J. Mol. Biol. 238:815-832(1994). MEDLINE=94238693; PubMed=8182750; Raghunathan S., Chandross R.J., Kretsinger R.H., Penington C.J., Rule G.S.; Eukaryota; Metazoa; Mammalia; Eutheria; GSTM2 UK GLL.. Homo sapiens (Human). "~ Metazoa; Chordata; 15-JUN-2002 (Rel. 41, Last annotation update) Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GSTM2-2) (GST class-mu STRAND STRAND Transferase; INIT\_MET MIM; EMBL; M63509; AAA60963.1; or send an email to license@isb-sib.ch). the European Bioinformatics Institute. Genew; between - !- SUBUNIT: HOMODIMER. -!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS). SEQUENCE FROM N.A. NCBI\_TaxID=9606 GSTM2 OR GST4. 138380 SWISS-PROT entry is copyright. It is produced through a centry is institute of Bioinformatics and the SMBL 3GTU; 1HNA; A39375; A39375 1HNC; 1 HNB; 2GTU; 02-MAR-99 HGNC:4634; GSTM2 31-JAN-94 31-JAN-94 29-JUL-99 31-JAN-94 Multigene 876554433322211 827550318527331720 GSTRNSFRASEM. Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. 887665443332221 410642919529422750 family; 3D-structure. .' There are no Allison T.J restrictions a collaboration on its

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Q RESULT 13 GTM2\_MOUSE B Best Loc Matches Query Match 01-APR-1990 (Rel. 14, Creace, 01-APR-1990 (Rel. 14, Last sequence update) 01-APR-1990 (Rel. 14, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST Clutathione S-transferase pmGT2) (GST 5-5). Kumat A., Note \_\_\_\_\_\_ "Genomic organization and characterization of the product of murine GSTM2 gene."; Gene 270:221-229(2001). -!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. -!- CATALYTIC ACTIVIII..... -!- SUBUNIT: HOMODIMER. -!- SUBCELLULAR LOCATION: Cytoplasmic. -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY. entities or send a This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s J. Biol. [2] TURN . STRAND TURN STRAND MEDLINE=90094327; PubMed=2689439; Townsend A.J., Goldsmith M.E., Pickett C.B., Cowna K.H.; "Isolation, characterization, and expression in Escherici two murine Mu class glutathione S-transferase cDNAs homo rat subunits 3 (Ybl) and 4 (Yb2)."; J. Biol. Chem. 264:21582-21590(1989). Eukaryota; Metazoa; Mammalia; Eutheria; NCBI\_TaxID=10090; TURN TURN HELIX HELIX TURN TURN TURN HELIX MEDLINE-21297196; Kumar A., Reddy E. STRAIN=3 SEQUENCE FROM N.A. Mus musculus (Mouse) SEQUENCE FROM N.A. P15626; GTM2\_MOUSE SEQUENCE HELIX STRAND HELIX HELIX F 56 Loca1 ω FPNLPYL 62 FPNAPYL 9 an 129/SvJ Similarity 6; Conser email 217 148 150 151 154 171 Conservative 178 191 128 147 130 90 114 117 861 A۶; STANDARD; 5 PubMed=11404019; Chordata; Rodentia; 149 151 151 189 197 113 115 118 127 215 147 146 143 141 license agreement license@isb-sib.ch 70.6%; 85.7%; 25613 MW; 0 Score 36; DB Pred. No. 7.7; 0; Mismatches Craniata; Vertebrata; ] Sciurognathi; Muridae; PRT; 25603A909482CA39 CRC64; . ch 217 (See http://www.isb-sib.ch/announce/ DB 7.7; There are no restrictions ng as its content is in AA 1; 1; Length 217 Escherichia coli of DNAs homologous to the Indels class-mu Euteleostomi;
Murinae; Mus and EMBL a collaboration MBL outstation ы for 0 Mus outstation commercial Gaps of no on its 0

REPRESENTATION CONCLUSION CONCLUSICON CONCLUS GTM2\_ B QY RESULT Query Match Best Local Matches PFam; PF00798; GST\_N; 1. Pfam; PF00043; GST\_C; 1. Pfam; PF00798; GST\_C; 1. PFINTS; PR01267. GTM2\_RAT P08010; 01-AUG-1988 01-AUG-1988 LT 14 RAT an anionic Yb subunit cDNA clone."; J. Biol. Chem. 261:13793-13799(1986). [5] SEQUENCE OF 24-217 FROM N.A. MEDLINE-86224097; PubMed-301 Ding G.J.-F., Ding V.D.-H., Pickett C.B.; Alin P., Mannervik B., Joernvall H.; "Cytosolic rat liver glutathione transferase 4-4. Primary structure of the protein reveals extensive differences between homologous glutathione transferases of classes alpha and mu."; Eur. J. Blochem. 156:343-350(1986). EMBL; J04696; AAA37706.1; --EMBL; AF319526; AAK28508.1; PIR; B34159; B34159. SEQUENCE OF 33-217 FROM N.A. MEDLINE-87008619; PubMed-3020050; Lai H.-C.J. Tu C.-P.D.; "Rat glutathione S-transferases supergene phenobarbital." J. Biol. Chem. STRAIN=Sprague-Dawley; Lai H.-C.J., Qian B., Grove G., Tu C.-P.D.; "Gene expression of rat glutathione S-transferases. conversion in the evolution of the Yb multigene fam. J. Biol. Chem. 263:11389-11395(1988). SEQUENCE FROM N.A. MEDLINE=88298790; Lai H.-C.J., Oian NCBI\_TaxID=10116; Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MGD; HSSP; P09488; 1GTU. SWISS-2DPAGE; P15626; "Rat liver glutathione cDNA clone and regulati MEDLINE=86192461; SEQUENCE GSTM2 Glutathione SEQUENCE Transterase; 4 Ξ 2 16-0CT-2001 InterPro; IPR004046; GST\_Cterm InterPro; IPR004045; GST\_Nterm NIT 56 3 FPNAPYL MET FPNLPYL MGI:95861; Gstm2 6; Conserv PR01267; GSTRNSFRASEM rase; Multigene family 3 (Rel. 08, Creat 3 (Rel. 08, Last 1 (Rel. 40, Last 2 S-transferase Y 217 AA; Conservative 62 ە 0 261:7952-7957(1986). regulation STANDARD; PubMed=3011803; g V.D.-H., Rodke PubMed=3699019; PubMed=3403534; 25585 MW; 70.6%; 85.7%; Created) Last sequence update) Last annotation update) rase Yb2 (EC 2.5.1.18) (Chain 4) (GST class-mu MOUSE S-transferases. ion.of the Ybl ar Rodkey 0 Score Pred. Craniata; Vertebrata; Sciurognathi; Muridae PRT; A3979D4435EF08AE CRC64; Mismatches No. J.A., 36; and 217 DNA sequence analysis nd Yb2 mRNAs by DB 7.7; Bennett C.D., AA family. ÷ Muridae; :: Length 217; family. Characterization Indels Evidence Euteleostomi; Murinae; Έ ----А.Ү.Н., 0 of a for Rattus Gaps gene Yb2 of 0

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RESULT 15 GTM3\_MCUSE ID GTM3\_CMUSE DT 01-FE DT 15-JU DE Gluta GN GSTM3 OS MUST OC Mamma OX NCBL RN GSTM3 OX NCBL RN MEDLI RA PEATS Q Sof Free Range Range Range Roce Coce Coce Coce Coce Coce Range Ran 망 Query Match Best Local : Matches P19639; 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Glutathione S-transferase Mu 3 (EC 2.5.1.18) (Glutathione S-transferase GT9.3). purification, molecular properties and odorant biotransformation. Biochem. J. 292:379-384(1993). -i- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. -i- FUNCTION: THE OLFACTORY GST MAY BE CRUCIAL FOR THE ACTITUM OF OLFACTORY PROCESS MOUSE PIR; PIR; Mus musculus (Mouse) Eukaryota; Metazoa; ( Mammalia; Eutheria; ) PIR; EMBL; EMBL; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way GTM3\_MOUSE SEQUENCE Pfam; Pf00043; GST\_C; 1.
Pfam; Pf02798; GST\_N; 1.
PRINTS; PR01267; GSTRNSE оŗ modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ MEDLINE=88330838; Pearson W.R., Rei CONFLICT Transferase; Multigene family; Olfaction. EMBL; ÷ ÷ ÷ -!- CATALYTIC ACTIVITY: RX + glutathione = STRAIN=Wistar; SEQUENCE FROM N.A. NCBI\_TaxID=10090; InterPro; InterPro; InterPro; HSSP; Ben-Arie N., MEDLINE=93277499; PubMed=8503873; SEQUENCE OF 56 FPNLPYL 62 **3 FPNAPYL** send LL; J02592; AAA4128 M13590; AAA4235 9L; J03914; AAA4235 9L; A25386; XURTC4. ; A26507; A26507; ; A265187; A26507; ; B26187; B26187. ; P09488; LGTU SUBUNIT: HOMODIMER ON HETERODIMER. SUBCELLULAR LOCATION: CYTOPLASMIC. MISCELLAUGOUS: RAT LIVER GLUTATHIONE S-TRANSPERASES (GST) CONSIST OF BINARY COMBINATIONS OF THREE MAJOR CLASSES OF SUBUNITS DESIGNATED: YA (25 KDA), YB (27 KDA) AND YC (28 KDA), MISCELLAUGOUS: YB SUBLASS SELECTIVELY BINDS STEROID MISCELLAUGOUS: YB SUBLASS SELECTIVELY BINDS STEROID SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY. Similarity 6; Conser an email to license@isb-sib.ch). IPR004046; GST\_Cterm. IPR004045; GST\_Nterm. IPR003081; GST\_mu. 146 217 AA; 1 - 21Conservative 9 Khen M., AAA41296.1; AAA41285.1; -. AAA42351.1; Reinhart J., STANDARD; TISSUE=Olfactory epithelium; GSTRNSFRASEM. PubMed=3417659; 146 Chordata; Rodentia; 70.6%; 85.7%; 25571 MW; .' Sisk S.C., 0; W -> S (IN REF. Pred. Score 36; Craniata; Vertebrata; Sciurognathi; Muridae; PRT ; -> S (IN REF. 2). F27B3D5831FF789F CRC64; Mismatches NO. 217 AA Anderson K.S., 7 DB 1; HX + R-S-glutathione (GST class-mu ۳. Length 217; biotransformation."; Indels Euteleostomi; ; Murinae; Mus Adler P.N.; ω 0 Gaps THE<u>,</u> QY Server a s Search completed: April Job time : 13 secs B Query Match Best Local S Matches 6 EMBL; PIR; B data and enzymatic properties."; proc. Natl. Acad. Sci. U.S.A. 82:7202-7206(1985). -!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES. -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione. Pfam; PF00043; GST\_C; 1
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PRINTS; PR01267; GSTRNS; HSSP; P04905; 2GST. MGD; MGI:106026; Gstm3. InterPro; IPR004046; GST\_Nterm. InterPro; IPR004045; GST\_Nterm. InterPro; IPR003081; GST\_mu. PIR; use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch). "Identification of three classes of cytosolic glutathione transfera-common to several mammalian species: correlation between structural "Tissue-specific induction of murine glutathione transferase mRNAs butylated hydroxyanisole."; J. Biol. Chem. 263:13324-13332(1988). [2] SEQUENCE Transferase; Multigene family. INIT\_MET 0 0 PLR; between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a This SWISS-PROT entry is copyright. It is produced through a collaboration ; Mannervik B., Alin P., Gu Warholm M., Joernvall H.; RNA. anticarcinogenic antioxidants. Cloning and measurement of messenger Pearson W.R., Windle J.J., Morrow J. "Increased synthesis of glutathione MEDLINE=86042634; PubMed=3864155; SEQUENCE OF 1-25. MEDLINE=83109018; SEQUENCE OF 1-40 FROM N.A. -!- SUBCELLULAR LOCATION: Cytoplasmic I- SIMILARITY: ω 56 Biol. Chem. 3 FPNAPYL 9 SUBUNIT: HOMODIMER. FPNLPYL B28946; B28946. E37520; E37520. B20831; B2083] J03953; AAA37748.1; Similarity 6; Conser 217 AA; Conservative 62 258:2052-2062(1983). BELONGS TO THE GST SUPERFAMILY. MU FAMILY. GSTRNSFRASEM. , 25, PubMed=6822548; 25570 MW; 70.6%; 85.7%; 2003, Guthenberg C., Jensson H., Tahir M.K., ALT\_INIT. Morrow J.F., Benson A.M., itathione S-transferases i Score 36; DB Pred. No. 7.7; 0; Mismatches 06:46:36 C4D8950EFEA585D8 CRC64; (See http://www.isb-sib.ch/announce/ ng as its content DB 1; .7 Usage glutathione transferase 1; Length 217; and the Indels in response to bу Talalay restrictions and EMBL outstation is

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RESULT 042223 RESULT Q15881 RA COCCOS OF TOTO Ŷ Q Db 昂 Query Match Best Local S Matches 9 Matches 01-JAN-1998 01-JAN-1998 01-JUN-2002 015881; 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, Trachemys scripta (Red-eared Eukaryota; Metazoa; Chordata; TWT1 Wilms tumor 042223; 042223 Q15881 SEQUENCE FROM Spotila L.m., Testudines; Cryptodira; NCBI\_TaxID=34903; Gessler M., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. Wilms tumor gene 1, exon InterPro; IPR000976; Wilms\_tumour InterPro; IPR000822; Znf\_C2H2. MEDLINE=92241883; Homo sapiens (Human) "The genomic NCBI\_TaxID=9606; 126 107 ω ຸ Р щ RMFPNAPYL 9 RMFPNAPYL 134 RMFPNAPYL 115 RMFPNAPYL Similarity 9; Conserv 9; 92241883; PubMed=1572653; M., Konig A., Bruns G.A.; omic organization and expression 12:807-813(1992). ш (TrEMBLrel. 05, (TrEMBLrel. 05, (TrEMBLrel. 21, Conservative Conservative PRELIMINARY; PRELIMINARY; IN.A. Hall protein. و S.E.; 100.0%; 100.0%; Testudinoidea; ۲ JOINED. JOINED. JOINED. JOINED. JOINED. NUCLEAR Created) Last sequ Last anno Last sequence update) Last annotation update) 0 0; Created) slider turtle) (Pseudemys scripta).
; Craniata; Vertebrata; Euteleostomi; Score 51; DE Pred. No. 0.0 ); Mismatches PRT; PRT ; Mismatches sequence up annotation (BY SIMILARITY). 390 446 Emydidae; DB 4; 0.093; of AA Ą update) Hominidae; update) 4; the WT1 0 0 Length 446 Trachemys Indels Indels Euteleostomi; gene. Ното 0 ۰. ,; Gaps Gaps 0 <u>,</u> RESULT Q90XX7 ID AC DT 01 Ъ QY · SQUERRER REPORT OF A CONSTRAINT OF A CONSTRAIN RESULT Q90XX8 멂 QY Query Match Best Local S Matches 8 Query Match Best Local Genome 44:455-462(2001). EMBL; AF334670; AAK52719.1; -. InterPro; IPR000976; Wilms\_tumour. InterPro; IPR000822; Znf\_C2H2. Pfam; PF00096; WT1: 1. Pfam; PF00096; Zf-C2H2; 4. ProDom; PD000003; Znf\_C2H2; 2. PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_4. PROSITE: PS00028; ZINC\_FINGER\_C2H2\_2; 4. PROSITE: PS00157; ZINC\_FINGER\_C2H2\_2; 4. SEQUENCE 386 AA; 43286 MW; 05622EF7642FC9E5 CR Matches InterPro: IPRO00976; Wilms\_tumour. InterPro: IPRO00976; Znf\_C2H2. Pfam; PPO2165; WT1; 1. Pfam; PPO2165; WT1; 1. ProDom; PDO0006; Zf-C2H2; 4. ProDom; PDO00003; Znf\_C2H2; 2. SMART; SM00355; ZnF\_C2H2; 4. PROSITE: PSO0028; ZINC\_FINGER\_C2H2\_1; 3. PROSITE: PSO0028; ZINC\_FINGER\_C2H2\_2; 4. PROSITE: PSO157; ZINC\_FINGER\_C2H2\_2; 4. SMART; SUS157; ZINC\_FINGER\_C2H2\_2; 4. SMART; SUS157; ZINC\_FINGER\_C2H2\_2; 4. SMART; SM0355; ZnF\_C2H2; 4. PROSITE: PSO028; ZINC\_FINGER\_C2H2\_2; 4. SMART; SM0355; ZNF\_C2H2; CH2\_2; 4. SMART; SM0355; ZNF\_C2H2; CH2\_2; 4. PROSITE: SUS157; ZINC\_FINGER\_C2H2\_2; 4. SMART; SM0355; ZNF\_C2H2; CH2\_2; 4. PROSITE: SM0355; ZNF\_C2H2; CH2\_2; 4. SMART; SM0355; ZNF\_C2H2; CH2\_2; 4. SMART; SM0355; ZNF\_C2H2; CH2\_2; 4. SMART; SM0355; ZNF\_C2H2; CH2\_2; 4. PROSITE: SM0355; ZNF\_C2H2; CH2\_2; 4. SMART; SM0355; ZNF\_C2H2; CH2\_2; CH2\_2 Q90XX7 Q90XX7; 01-DEC-2001 01-DEC-2001 01-DEC-2001 01-JUN-2002 Q90XX8; Oncorhynchus.mykiss (Rainbow trout) (Salmo gairdneri). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygli; Neopterygli; Telcostei; Euteleostei; Protacanthopterygli; Salmoniformes; Salmonidae; Oncorhynchus. "Expression of a new RNA-splice isoform of WT1 in developing kidney/gonadal complexes of the turtle, Trachemys scripta."; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. -i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). EMBL; AF019779; AAB70832.1; -. gene. SEQUENCE FROM N.A. MEDLINE=21337607; PubMe Brunelli J.P., Robison WT-T1A. Wilms' tumor 112"Ancient and NCBI\_TaxID=8022 HSSP; P08046; 1AAY 109 4 თ 1 RMFPNAPYL ш RMFSNAPYL RMFPNGPYL 117 RMFPNAPYL Similarity 8; Conserv Similarity 8; Conservat 1 (TrEMBLrel. 1 (TrEMBLrel. 2 (TrEMBLrel. 2 suppressor (TrEMBLrel. Conservative PRELIMINARY; PRELIMINARY; Conservative recent 120 و ف PubMed=11444705; bison B.D., Thorgaard G.H.; duplications 92.2%; 88.9%; 84. 88. 19, 19, 21, 1a. 19, .98 98 Created) Last sequence up Last annotation 0; Created) <u>,</u> Score 43; Pred. No. Score 47; DB 13; Pred. No. 0.48; PRT; PRT ; ced. No. 2.8; Mismatches 05622EF7642FC9E5 CRC64; Mismatches of the 388 386 rainbow trout Wilms' Ą Ŗ update) 13; update) Zinc-finger. 7C2 CRC64; **!**: ... Length 386; Length 390; Indels Indels 0 0 tumor Gaps Gaps

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RESULT Q91657 밇 QУ Query Match Best Local Matches PROSITE; PS00 PROSITE; PS50 DNA-binding; Oncogene •!- SUBCE Carroll T. Submitted EMBL; WT1. pfam; PF02165; WT1; 1.
pfam; PF00096; zf-C2H2; 4.
probom; PE000905; znf\_C2H2; 2.
ProsITE; PS00028; zINC\_FINGER\_C2H2\_1;
PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2;
PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; gene. InterPro; IPR000976; Wilms\_tumour. InterPro; IPR000922; Znf\_CZH2. Pfam; PF00265; WT1; 1. Pfam; PF00096; zf-C2H2; 4. Xenopus laevis (African clawe Eukaryota; Metazoa; Chordata; Amphibia; Batrachia; Anura; M 01-NOV-1996 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. WILMS' tumor suppressor Q91657; 01-NOV-1996 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Beukaryota; Metazoa; Chordata; Craniata; Euteleostei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncori 01-1007-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Wilms' tumor suppressor SMART ; ProDom; PRINTS; HSSP; EMBL; MEDLINE=96068905; pubMed=7478606; Kent J., Coriat A.M., Sharpe P.T. "The evolution of WT1 sequence an vertebrates."; SEQUENCE OF 289-370 FROM N.A. TISSUE=MESONEPHROS; SEQUENCE NCBI\_TaxID=8355; Xenopodinae; Q91657 SEQUENCE EMBL; AF334671; AAK52720.1; -Genome 44:455-462(2001) NCBI\_TaxID=8022; WT-T1B InterPro; IPR000976; Wilms\_tumour. InterPro; IPR000822; Znf\_C2H2. Ξ 112 RMFSNAPYL 120 ucogene 11:1781-1792(1995). -- SUBCELLULAR LOCATION: NUC: NBL; U42011; AAB53152.1; -. BL; X85733; CAA59738.1; -. SP; P08046; LAAY. .erbro. გ ч RMFPNAPYL SM00355; . Similarity 8; Conserv PR00048; ZINCFINGER. PD000003; Znf\_C2H2; SM00355; ZnF\_C2H2; 4. E FROM N.A. T.J., Vize P. ed (JAN-1996) -4 y; Zinc-finger.
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QY 2 MFPNAPYL 9          Db 115 MLPNAPYL 122 RESULT 12 Q91030	atch 31 Similarity 87.5%; Pred. No. 7.9; 7; Conservative 0; Mismatches 1;		OG Plasmid megaplasmid. OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group; OC Ralstonia. OX NCBI_TaxID=305; RN [1] RP SEQUENCE FROM N.A. RC STRAIM=GMI1000; RX MEDLINE=21681879; PubMed=11823852;	Q8XP Q8XP 01-M 01-M 01-M Hypo RSP1 RSP1	rt 9 11 96	FT NON_TER 1 1 FT NON_TER 250 250 SQ SEQUENCE 250 AA; 27236 MW; 90FA4B0B5FF59F6A CRC64; Query Match 78.4%; Score 40; DB 13; Length 250; Best Local Similarity 77.8%; Pred. No. 6.9; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	(CBF (1) SEQU SEQU Deve EMBL Inter Pfar	AC 098SJ4; DT 01-JUN-2001 (TrEMBLrel. 17, Created) DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE Wilms' tumor suppressor (Fragment). GN WTL OS Brachydanio rerio (Zebrafish) (Zebra danio) OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

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pROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.
DNA-binding; Metal-binding; Zinc\_Finger.
SEQUENCE 417 AA; 46957 MW; 47BBF7F6448E7F6C CRC64; PRINTS; PR00049; WILMSTUMOUR. Prodom; PD000003; Znf\_C2H2; 2. SMART; SM00355; ZnF\_C2H2; 4. InterPro; IPR000976; Wilms\_tumour. InterPro; IPR000822; Znf\_CZH2. Pfam; PF02165; WT1; 1. Pfam; PF02066; Zf-CZH2; 4. "Chicken counterpart of Wilms' submitted (OCT-1999) to the EMI EMBL; AB03634; BAA94794.1; -HSSP; P08046; LAAY WT1(+KTS) WT1(+KTS) protein. Q918A0; 01-OCT-2000 (TrEMBLrel. 01-OCT-2000 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Q918A0 PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4. DNA-binding; Metal-binding; Zinc-finger. SEQUENCE 414 AA; 46641 MW; 17EB22F8B Smith S.I., Down TISSUE=OVARY; SEQUENCE FROM N.A NCBI\_TaxID=9031; Gallus Archosauria; Aves; SEQUENCE FROM N.A Kudo 109 109 14 Local Local 1 RMEPNAPYL 1 RMFPNAPYL RMFPQRPYL 117 RMFPQRPYL 1 Similarity
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A;Note: C;Geneti Cell 60, 509-520, 1990 A;Title: Isolation and characterization of A:Poference number: A34673; MUID:90150277; A; Molecule type: mRNA A; Residues: 'SRORPHPGALENPTACPLPHFPPSLPPTHSPTHPPRAGTAAQAPGPRRLLAAILDFLLLQDPASTCVPEPASQH1 A; Cross-references: EMBL:X51630; NID:g37977; PIDN:CAA35956.1; PID:g37978 R;Call, K.M.; Glaser, T.; Ito, C.Y.; Buckler, A.J.; Pelletier, J.; Haber, D.A.; Rose, E. A;Cross-references: GB:X61631; GB:S99414; NID:g37981; PIDN:CAA43819.1; PID:g825731 A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiat A;Note: sequence extracted from NGBI backbone (NCBIN:99414, NCBIN:99422, NCBIN:99479, NC A;Note: the sequence in GenBank entry HSWTGEEX1, release 113.0, PIDN:CAA43819.1 differs R;Gessler, M.; Poustka, A.; Cavenee, W.; Neve, R.L.; OrKin, S.H.; Bruns, G.A.P. Nature 343, 774-778, 1990 R;Gessler, M.; Konig, A.; Bruns, G.A. Genomics 12, 807-613, 1992 A;Title: The genomic organization and expression of the A;Reference number: A38080; MUID:92241883; PMID:1572653 A;Accession: A38080; A;Accession: A38080; A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 355-365,'H',367-377 <PEL> A;Cross-references: GB:S61513; NID:g237599; A;Contents: annotation; alternative splicing R;Phelan, S.A.; Lindberg, C.; Call, K.M. Cell Growth Differ. 5, 677-686, 1994 A;Title: Wilms' tumor gene, WT1, mRNA is down-regulated A;Reference number: I38504; MUID:94368704; PMID:8086342 A;Molecule type: mRNA A;Residues: 85-749,267-364,'F',366-386,'T',388-407,411-449 <CAL> A;Cross-references: GB:M30393; NID:g340381; PIDN:AAA36810.1; PID:g340382 A;Cross-references: GB:M30393; NID:g340381; PiDN:AAA36810.1; PID:g340382 A;Haber, D.A.; Sohn, R.L.; Buckler, A.J.; Pelletier, J.; Call, K.M.; Housman Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991 A;Title: Alternative splicing and genomic structure of the Wilms tumor gene A;Reference number: A56411; MUID:92052142; PMID:1658787 C;Species: Homo sapiens (man) C;Date: 31-Dec-1993 #sequence\_revision C;Accession: A38080; S08273; A34673; I: A;Residuq<u>a</u>; 'MGHHHHHHHHHHSGHIEGRHM',301-364,'F',366-386,'T',388-407,411-449 A;Cross-references: GB:S75264; NID:g896246; PIDN:AAB33443.1; PID:g896247 A;Reference number: I58315; A;Accession: I58315 R;Hamilton, T.B.; Barilla, K.C.; Romaniuk, P.J. Nucleic Acids Res. 23, 277-284, 1995 A;Tile: High affinity binding sites for the Wilms' tune A;Reference number: I58315; MUID:95166649; PMID:7862533 A;Reference number: I52811; A;Accession: I52811 A;Cross-references: EMBL:U06486; NID:g473563; PIDN:AAA62865.1; PID:g458432 R;Pelletier, J.; Bruening, W.; Kashtan, C.E.; Mauer, S.M.; Manivel, J.C.; Cell 67, 437-447, 1991 A;Title: Germline mutations in the Wilms' tumor suppressor gene are associ A; Molecule type: DNA A; Residues: 1-18 <PHE> A;Reference number: I38504; A;Accession: I38504 A;Reference number: A;Accession: A34673 A;Title: Homozygous deletion in Wilms tumours of a zinc-finger gene identified by A;Reference number: S08273; MUID:90158822; PMID:2154702 A;Accession: S08273 B Ŷ A; Molecule type: mRNA A;Status: translated from A; Note: mutant form A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-449 <GES1> A; Molecule type: DNA Wilms tumor A38080 Genetics: 125 this sequence is H RMFPNAPYL RMFPNAPYL susceptibility protein WT1 -133 9 engineered GB/EMBL/DDBJ in the Wilms' t MUID:92005721; .on 31-Dec-1993 #text\_change 20-J
I38504; I52811; I58315; A56411; human ; PMID:1655284 a zinc finger PMID:2154335 PIDN:AAB20109.1; tumour WT1during induction of erythroid polypeptide gene suppressor gene PID:g237600 20-Jun-2000 5411; S26286 associated Housman, protein .Striegel, at WT1. the <HAM> U WT1 with Ē human chrom J.E. abr â

AD1343 A;Title: Isolation, characterization, and expression A;Reference number: A39692; MUID:91141522; PMID:16717 A;Accession: A39692 Wilms' tumor protein analog, WT1 - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 16-Feb-1997 C;Accession: A39592 0 A;Reference number: A;Accession: AD1343 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; 1 C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 망 Q R;Buckler, A.J.; Mol. Cell. Biol. QY A;Note: mRNA transcripts containing both alternatively spliced regions are the most a C;Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zine finger F;1-449/Product: Wilms tumor susceptibility protein WT1, splice form 1 #status predic F;1-407,411-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #statu F;1-249,267-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #statu F;1-249,267-407,411-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #statu A;Gene: A, Experimental source: A; Molecule type: DNA A; Residues: 1-213 <GLA> ok, c A; Authors: Kreft, J.; Kuhn, M.; Science 294, 849-852, C;Accession: AD1343 hypothetical protein lmo2148 [imported] - Listeria monocytogenes (strain RESULT C;Keywords: alternative A;Molecule type: mRNA A;Residues: 1-449 <BUC> A39692 망 A; Map position: A; Introns: 148/ A; Cross-references: A;Status: preliminary A; Title: Comparative A;Cross-references: GB:M55512 A;Status: preliminary RESULT A;Gene: GDB:WT1 A;Cross-references: GDB:120496; Genetics: Query Match Matches Query Match Query Match Best Local : Matches Best Local Best Matches Jones, .; Schlueter, 126 RMFPNAPYL 134 126 RMFPNAPYL 134 σ Local Local **1 RMEPNAPYL 9** 1 RMFPNAPYL 9 lmo2148 L.M.; tion: 11p13-11p13 148/1; 189/1; 223/2; 249/2; 266/2; 298/3; 349/1; 379/1; 410/1 Similarity 9; Conserv Similarity Similarity 9; Conserv Pelletier, J.; Haber, D.A.; Glaser, 11, 1707-1712, 1991 Karst, Conservative Conservative Conservative T.; Simoes, N.; Tierrez, ve genomics of Listeria s c: AB1077; MUID:21537279; GB:NC\_003210; PIDN:CAD00226.1; ce: strain EGD-e q splicing; 100.0%; 80.48; 100.08; 100.0%; Kunst, F.; Kurapkat, N.; Tierrez, A.; Vazqu OMIM:194070 0 Score 41; Pred. No. 0 0 DNA binding; transcription regulation; Score 51; DB 2; Pred. No. 0.054; Score 51; DB 2; Pred. No. 0.054; Mismatches Mismatches Mismatches species. ; PMID:11679669 expression of PMID:1671709 DB .9 ; pkat, G.; Madueno, Vazquez-Boland, J ູ່ 2 2; A.; Baquero, 1 Dussurget, O.; #text\_change PID:g16411618; GSPDB:GN00177 0 <u>,</u> 0 Length Τ.; Length 449; Length 449; Indels Indels Indels the Housman, 213; murine F) ч 27 - Nov - 2001 0 Entian, 0 0 . E . . 0 Wilms' Berche, Gaps Gaps Gaps Maitournam, Voss, H.; W k.D.; I EGDtumor suppre tumor Η.; æ 0 0 ò ; Bloec Fsihi, Wehla gene 2

RESULT 8 C71375 conserved hypothetical integral membrane protein TP0033 - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999 C;Accession: C71375	QY 1 RMFPNAPY 8 1:111:11 Db 151 RVFPNSPY 158	Query Match 78.4%; Score 40; DB 1; Length 262; Best Local Similarity 75.0%; Pred. No. 3.8; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	C;Superfamily: conserved hypothetical protein H10177	A;Accession: G64144 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A:Molecule type: DNA	A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMTD:7547800	R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.	664144 hypothetical protein HI0177 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae C;Date:10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000 C;Accession: 664144	DD 67 FPNAPYL 73	PPNAPYL 9	Conservative O. Mismatches O. Todole O. Cons	Cross-refe Experiment Genetics: Gene: lin2	A;ACCeSSION: AHI/L3 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-213 <gla></gla>	A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669	H1713 Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Ber ernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian ; Karst, U. 49-852, 2001	AHI713 hypothetical protein homolog lin2252 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C:Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text chance 27-Nov-2001	RESULT 6	OY 3 FPNAPYL 9 Db 67 FPNAPYL 73
A;Reference number: AB1097; MULD:21393203; PMLD:11/39840 A;Accession: AB2195 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-214 <kur> A;Cross-references: GB:BA000019; PIDN:BAB74812.1; PID:g17132207; GSPDB:GN00179 A;Cross-references: GB:BA000019; PIDN:BAB74812.1; PID:g17132207; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:</kur>	Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yanada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium h: Deference number: Ap1007. MITC, 21505205. NNTP.1175004.	C; Accession: AB:195 Y : Work of the content of the	RESULT 10 AB2195 serine esterase [imported] - Nostoc sp. (strain PCC 7120)	75 M	ocal Similarity /5.0%; ss 6; Conservative 7 MEDNADVI 9	02 h 74.5%; Score 38;	A;Molecule type: DNA A;Residues: 1-205. <sto> A;Cross-references: GB:AE004550; GB:AE004091; NID:g9947122; PIDN:AAG04591.1; GSPDB:GN A;Cross-rimental source: strain PAO1 C:Genotics:</sto>	A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: F83495 A;Status: preliminary	adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L ; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000	Pseudomonas aeruginosa Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-bec- 1: F83495	RESULT 9 F83495 probable hydrolase PA1202 [imported] – Pseudomonas aeruginosa (strain PAO1)	QY 3 FPNAPYL 9 IIIIII: DD 63 FPNAPYI 69	Ouery Match 76.5%; Score 39; DB 2; Length 203; Best Local Similarity 85.7%; Pred. No. 4.4; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	A;Cross-references; GB:AE001188; GB:AE000520; NID:g3322282; PIDN:AAC65028.1; PID:g332 A;Cross-references; GB:AE001188; GB:AE000520; NID:g3322282; PIDN:AAC65028.1; PID:g332 A;Experimental source: strain Nichols C;Genetics: A;Gene: TP0033	A;Accession: C71375 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA	Science 281, 375-388, 1998 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876	R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M they. L.: Weidman. J.: Smith. H.O.: Venter. J.C.

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Qy I RMFPNAPYL 9 Db 201 RMSPNSPYV 209 C RESULT 13 S33558	Query Match 72.5%; Score 37; DB 2; Length 466; Best Local Similarity 66.7%; pred. No. 27; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	ced 56K protein	pr. J. Biochem. Title: The inte pha inducibilit Reference numbe Accession: S422 Status: prelimi	tein - Chinese hamster Dricetulus griseus (Chinese hamster) reb-1995 #sequence_revision 06-Feb-1995 #text_change : \$42210	QY 1 RMFPNARY 8 Db 349 RMFPNARY 356 RESULT 12	Query Match 74.5%; Score 38; DB 2; Length 581; Best Local Similarity 87.5%; Pred. No. 22; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Cross-refe Genetics: Map positi		Rooney, T.; Rowley, D.; Sakano, H.un, Z.Y., Buros, S.J., Buros, Y.J., Rowley, D.; Sakano, H.un, Z.Y., Southwick, A.M.; Sun, H.; Tal Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal J. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.; Sauence and analysis of chromosome 1 of the plant Arabidopsis.	R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 200 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Hunter, J.L.; Jenkins, J.; Sohnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.	- Arabidopsis thaliana idopsis thaliana (mouse-ea 2001 #sequence_revision 02	QY 2 MEPNAPY 8 :11111 DD 56 VEPNAPY 62	A;Gene: all3113 Query Match 74.5%; Score 38; DB 2; Length 214; Best Local Similarity 85.7%; Pred. No. 7.3; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
SULT 15 7463 utathione transfer Species: Mus muscu Species: 22-Nov-1993	RMEPNAPYL 9        :  RCEPNOPEL 345	Query Match 72.5%; Score 37; DB 2; Length 1232; Best Local Similarity 66.7%; Pred. No. 79; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	A;Map position: 5412.2-5413 C;Keywords: appotosis; ATP: glycoprotein; nucleotide binding; P-loop; transmembrane p F;94-110/Domain: transmembrane #status predicted <tmm1> F;470-477/Region: nucleotide-binding motif A (P-loop) F;479-46//Domain: transmembrane #status predicted <tmm2> F;479/Binding site: ATP (Lys) #status predicted F;618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted</tmm2></tmm1>	A;Residues: 1-1232 <roy> A;Cross-references: GB:U19251 C;Genetics: A;Gene: GDB:SMAG; SMA A;Cross-references: GDB:120378; OMIM:600354; OMIM:253300</roy>	<pre>le Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A (7-178, 1995 'he gene for neuronal apoptosis inhibitory protein is partially de: 'ne number: A55478; MUID:95112344; PMID:7813013 'n: A55478</pre>	C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001 C;Accession: A55478 R;Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; Baird	apoptosis	QY 1 RMFPNAPYL 9 1:   :    Db 773 RLSPNSPYL 781	Query Match 72.5%; Score 37; DB 2; Length 854; Best Local Similarity 66.7%; Pred. No. 52; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	A;Introns: 14/2; 68/1; 129/3; 151/3; 182/1; 255/3; 361/2; 660/1; 790/3 C;Keywords: alternative intilators F;1-854/Product: unc-33 protein (long form) #status predicted <mat1> F;176-854/Product: unc-33 protein (intermediate form) #status predicted <mat2> F;332-854/Product: unc-33 protein (short form) #status predicted <mat3></mat3></mat2></mat1>	Cross-refe Accession: Molecule t Residues: Cross-refe		unc-33 protein - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 07-Apr-1994 #sequence_revision 02-Jun-1994 #text_change 21-Jul-2000 C;Accession: S33558; S33559; S24643; S24644 R;Li, W.; Herman, R.K.; Shaw, J.E.	

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C;Accession: S17463 R;Hayes, J.D.; Kerr, L.A.; Peacock, S.D.; Cronshaw, A.D.; McLellan, L.I. Biochem. J. 277, 501-512, 1991 A.Pitle: Hepatic glutathione S-transferases in mice fed on a diet containing the anticar adient elution of the glutathione-Sepharose affinity matrix. A;Reference number: S16933; MUID:91315425; PMID:1859377 A;Accession: S17463 A;Nolecule type: protein A;Residues: 1-38;39-64;65-85 <HAY> C;Superfamily: glutathione transferase C;Keywords: blocked amino end; dimer; transferase Db QY Search completed: April 25, 2003, 06:52:27 Job time : 46 secs Query Match70.6%;Score 36;DB 2;Length 85;Best Local Similarity85.7%;Pred. No. 6.3;.Matches6;Conservative0;Mismatches1; Fri Apr 25 08:06:21 2003 3 FPNAPYL 9 ||| ||| 23 FPNLPYL 29 4+ 7 0; Gaps us-09-625-963-1.open.rpr 0; • •

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